

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 05:44:31 ; Search time 6820 Seconds
(without alignments)
11377.025 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggagag.....tatggcatgctcgagctgcg 1365

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sta.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1365	100.0	1365	6	AR606281 Sequence
2	1365	100.0	1365	6	AX490719 Sequence
3	585.8	42.9	1380	15	AV325817 Lycopersi
4	584.2	42.8	1747	15	U49113 Oryza sativ
5	583.2	42.7	1417	15	AB039916 Vicia fab
6	582.8	42.7	1563	15	AK072676 Oryza sat
7	581.8	42.6	1376	15	AK071838 Oryza sat
8	581	42.6	1497	15	AJ298829 Fagus syl
9	575.4	42.2	1475	15	AB039917 Vicia fab
10	575	42.1	1370	15	AF107464 Hevea bra
11	574.2	42.1	1264	15	AF107464 Hevea bra
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ALIGNMENTS

RESULT 1	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
LOCUS	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
DEFINITION	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
ACCESSION	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
VERSION	AR606281.1	GI:56658183	1365 bp	DNA	linear	EC-2004
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1365)					
AUTHORS	da Costa e Silva.O., Bohnert,H.J., van Thielens,N., C					
TITLE	Phosphatase stress-related proteins and methods of u					
JOURNAL	Patent: US 6818805-A 8 16-NOV-2004;					
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Db	61	GTTGGGCAATCGCTCATATGCAGATGTAGACCGGAGATAGACGAGC				TG 120
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Db 601 CCGAGCCCTAGATCGTATTCAAGAAAGTGC CGACAGGCGCGATGTGTGATCTACTCTG 660

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RESULT 2

LOCUS AX490719 1365 bp DNA linear

DEFINITION Sequence 8 from Patent WO0246442.

ACCESSION AX490719

VERSION AX490719.1 GI:22323691

KEYWORDS

SOURCE Physcomitrella patens

ORGANISM Physcomitrella patens

REFERENCE 1 da Costa,E.S., Bohnert,H.J., Ishitani,M., van Thiele: Chan,R.

AUTHORS

TITLE Phosphatase stress-related proteins and methods of u.

JOURNAL Patent: WO 0246442-A 8 13-JUN-2002;

BASEL Plant Science GmbH (DE)

FEATURES

Location/Qualifiers

1..1365

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1365; Conservative 0; Mismatches 0; Indels 3 0;

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Db 61 GGTGGGCAATCGCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 1G 120

Qy 121 CAACCGGTTGTCGAGTTGGAGGTGAAGAACTATGTATCAAGCTCGGA 3T 180

Db 121 CAACCGGTTGTCGAGTTGGAGGTGAAGAACTATGTATCAAGCTCGGA 3T 180

Qy 181 GGAGAGTGGAACTGACGCCCGTGAAGTGTCTGTCAAGTTTTCGGGTG 3G 240

Db 181 GGAGAGTGGAACTGACGCCCGTGAAGTGTCTGTCAAGTTTTCGGGTG 3G 240

Qy 241 CCAGTTTCATGATCTCATCGAGCTTTCCGCATAGGAGGCAAGCGCCCG 3A 300

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RESULT 3
LOCUS AY325817
DEFINITION Lycopersicon esculentum protein phosphatase 2A catalytic subunit
(Pp2Ac1) mRNA, complete cds.
ACCESSION AY325817
VERSION AY325817.1 GI:34398260
KEYWORDS Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1380)
REFERENCE He,X., Anderson,J.C., Pozo Od.O., Gu,Y.Q., Tang,X. and Martin,G.B.
AUTHORS Silencing of subfamily 1 of protein phosphatase 2A catalytic
TITLE subunits results in activation of plant defense responses and
localized cell death
JOURNAL Plant J. 38 (4), 563-577 (2004)
```

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PUBMED 15125764
REFERENCE 2 (bases 1 to 1380)
AUTHORS He,X., Anderson,J.C., del Pozo,O., Gu,Y.-Q., Tang,X.
Martin,G.B.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-2003) Boyce Thompson Institute, Cc
University, Tower Road, Ithaca, NY 14853, USA
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Db 680 CAATGTTTGAAGTATTTCACTGATCTCTTTGATTTATCACTATGACGG -GA 739
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Db	1100	AAACATGGAGCAGAAATTTCTTCAGTTTGACCCAGCTCCACACAGATTTGAGCCTGATAC	1159
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Db	1160	TACAAGGAAGACTCCAGACTACTTCTTGTGAATC	1192
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OSU49113			
LOCUS			
DEFINITION			
Oryza sativa protein phosphatase 2A mRNA, complete cds.			
ACCESSION			
U49113			
VERSION			
U49113.1 GI:1218053			
KEYWORDS			
SOURCE			
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Oryza sativa (indica cultivar-group)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
Ehrhartoideae; Oryzeae; Oryza.			
1. (bases 1 to 1747)			
Chang, M., Wang, B., Chen, X. and Wu, R.			
Molecular characterization of catalytic-subunit cDNA sequences			
encoding protein phosphatases 1 and 2A and study of their roles in			
the gibberellin-dependent Osamy-c expression in rice			
Plant Mol. Biol. 39 (1), 105-115 (1999)			
10080713			
REFERENCE			
AUTHORS			
TITLE			
Direct Submission			
JOURNAL			
Submitted (13-FEB-1996) Men-Chi Chang, Plant Biology, Room 317			
Biotech. Building, Cornell University, Ithaca, NY 14850, USA			
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CDS			
source			
Oryza sativa (indica cultivar-group)			
Oryza sativa (indica cultivar-group)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
Ehrhartoideae; Oryzeae; Oryza.			
1. (bases 1 to 1747)			
Chang, M., Wang, B., Chen, X. and Wu, R.			
Molecular characterization of catalytic-subunit cDNA sequences			
encoding protein phosphatases 1 and 2A and study of their roles in			
the gibberellin-dependent Osamy-c expression in rice			
Plant Mol. Biol. 39 (1), 105-115 (1999)			
10080713			
REFERENCE			
AUTHORS			
TITLE			
Direct Submission			
JOURNAL			
Submitted (13-FEB-1996) Men-Chi Chang, Plant Biology, Room 317			
Biotech. Building, Cornell University, Ithaca, NY 14850, USA			
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RESULT 5
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LOCUS      AB039916          1417 bp      mRNA      linear      PLN 15-MAR-2000
DEFINITION Vicia faba vFP2Ac-1 mRNA for type 2A protein phosphatase-1,
complete cds.
ACCESSION AB039916
VERSION   vFP2Ac-1; type 2A protein phosphatase-1.
KEYWORDS Vicia faba (fava bean)
SOURCE    Vicia faba
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Vicia.
REFERENCE 1 (bases 1 to 1417)
AUTHORS   Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.
TITLE     Type 2A protein phosphatase from guard cells of Vicia faba
JOURNAL   Published Only in Database (2000)
REFERENCE 2 (bases 1 to 1417)
AUTHORS   Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.
TITLE     Direct Submission
JOURNAL   Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu University,
Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka
810-8560, Japan (E-mail: toshiro@box.nc.kyushu-u.ac.jp,
Tel: 81-92-726-4763 (ex. 4763), Fax: 81-92-726-4644)
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DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:JC
insert sequence.
ACCESSION AB072676
VERSION   AK072676.1 GI:32982699
KEYWORDS  FLI cDNA; CAP trapper.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS   The Rice Full-Length cDNA Consortium, National Insti
Agrobiological Sciences Rice Full-Length cDNA Projec
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooi
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K
Ohtsuki, K., Shihiki, T., Foundation of Advancement c
Science Genome Sequencing & Analysis Group, Otsomo, Y
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Ni

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Ikedo, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
12869764
2 (bases 1 to 1563)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
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Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan [E-mail: skikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007]
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Sato, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.
PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
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Yoshimura, A., Mateubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hiramoto, K.,
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FEATURES
source

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ACCESSION AJ298829
VERSION AJ298829.1 GI:10638984
KEYWORDS pp2A-1 gene; protein phosphatase 2A.
SOURCE Fagus sylvatica (European beech)
ORGANISM Fagus sylvatica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Gonzalez,M., Nicolas,C., Lorenzo,O., Nicolas,G. and Rodriguez,D.
Characterization and expression of a protein phosphatase type 2A
regulated by GA3 in dormant Fagus sylvatica seeds
Unpublished
2 (bases 1 to 1497)
Direct Submission
Nicolas,C.
Submitted (02-OCT-2000) Nicolas C., Fisiologia Vegetal, Universidad
de Salamanca, Plaza Doctores de la Reinas/n, 37007 Salamanca, SPAIN
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Query Match 42.6%; Score 581; DB 15; Length 149
Best Local Similarity 74.8%; Pred. No. 1.le-163; Indels
Matches 728; Conservative 0; Mismatches 245;
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ACCESSION	AB039917			
VERSION	AB039917.1	GI:7248360		
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SOURCE	Vicia faba (fava bean)			
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	Vicia			
REFERENCE	(bases 1 to 1475)			
AUTHORS	Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.			
TITLE	Type 2A protein phosphatase from guard cells of Vicia faba			
JOURNAL	Published Only in DataBase (2000)			
REFERENCE	2 (bases 1 to 1475)			
AUTHORS	Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.			
TITLE	Direct Submission			
JOURNAL	Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu University,			
	Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka			
	810-8560, Japan (E-mail:toshirch@box.nc.kyushu-u.ac.jp,			
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AUTHORS Shin,D.H. and Han,K.-H.
 TITLE Direct Submission
 JOURNAL Submitted (17-NOV-1998) Kumho Life and Environmental Science Laboratory, 572 Seangam-Dong, Kwangsan-Gu, Kwangju 506-712, Korea

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LOCUS
DEFINITION
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VERSION
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AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT

FEATURES
source
CDs

ORIGIN
Query Match
Best Local Similarity
Matches

Query
Db

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VERSION AY059847.1 GI:16648954
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; eudicotyledons: core e
rosids: eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1343)
Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kan
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pha
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (22-OCT-2001) DNA Sequencing and Technolo
Stanford University, 855 California Avenue, Palo Alt
USA
e-mail for correspondence: arab@sequence.stanford.ed

RIKEN Genomic Sciences Center (GSC) members carried
collection and clustering of RAPL cDNAs (RAPL cDNA :
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M.
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members ca
sequencing and annotation of the RAPL cDNAs: Nguyen,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chu
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shir
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) con
equally to this work. Shinozaki,K. (RIKEN GSC) and
(SSP/Stanford) contributed equally to this work as

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Location/Qualifiers

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CDS

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ORGANISM Arabidopsis thaliana
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1092)
AUTHORS Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
TITLE Submitted (26-MAR-2002) DNA Sequencing and Technology Center,

Stanford University, 855 California Avenue, Palo Alto, USA
e-mail for correspondence: arab@sequence.stanford.edu
RIKEN Genomic Sciences Center (GSC) members carried collection and clustering of RAFL cDNAs (RAFL cDNA: Arabidopsis Full-length cDNA): Seki,M., Narusaka,M Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, Hayashizaki,Y. and Shinozaki,K.
The Salk, Stanford, PGSC (SSP) Consortium members carried sequencing and annotation of the RAFL cDNAs: Southw. Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., P. Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chu Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) equally to this work. Shinozaki,K. (RIKEN GSC) and (SSP/Stanford) contributed equally to this work as ; Location/Qualifiers
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Best Local Similarity 76.4%; Pred. No. 1.5e-161;
Matches 704; Conservative 0; Mismatches 217; Indels
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Qy 251 GATCTCATCGAGCTTTTCCGCATAGGAGCGCCCGCCGACCACTA 310
Db 181 GACCTTATGAGCTTTTCTGTATCGTGGCAACGCTCTCTGATACTA 240
Qy 311 GCGCCTATGAGTGTGGATATATTCTGTGAGAGATGTGTGCTCTT 370
Db 241 GGAGACTATGATCGTGGCTACTATTTCAGTAGAGACAGTTTCTCTATT 300
Qy 371 AAGTGGGTATAGGATAGGATCAATCTTTCGAGGGAACCAACGAGAG 430


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Db 948 TTATACCTTTGGACAGGATATAGCATCTCAATTAATCACCAATGGTCTCACCTGAT 1007
Qy 772 TGCACGTGCTCACCGTCTGTGATGGAAGGATACAAATGGTGCCAGGATAAAAATGTTGT 831
Db 1008 TTCTAGAGCTCATCAGCTTGATGAGGGTTTCAATGGTGTGAGGATAGAATGTTGT 1067
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RESULT 15
LOCUS AY087557 1261 bp mRNA linear PLN 14-APR-2003
DEFINITION Arabidopsis thaliana clone 36621 mRNA, complete sequence.
ACCESSION AY087557
VERSION AY087557.1 GI:21406295
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1261)
Haas,B.J., Volkovsk,N., Town,C.D., Troughan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
12093376
2 (bases 1 to 1261)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1261)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the ws or llaer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
Location/Qualifiers
1. .1261
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="36621"
153. .1073
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FCLHGGSPLSDTLNLSIRDIOEVPHEGMDLLWSDDPDR:
QDIAQTQHNHNLGLISRAHQLVMEGYNWCOEKNNVTVFSAPN
EKMBQNFLOPDPAPQVPEPDTTRKTPDYFL"

ORIGIN
Query Match 41.1%; Score 561; DB 15; Length 126.
Best Local Similarity 75.6%; Pred. No. 1.2e-157;
Matches 696; Conservative 0; Mismatches 225; Indels
3 0;

Qy 71 ATGCGGTCAATGATGATAGACCGGAGATAGAGCAGCTGTCGAGTG 130
Db 153 ATGCGGTCAACCGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTG 212
Qy 131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGACGATCTTGGT 190
Db 213 GGTGAAGCAGACGTAAGATCTTTGGATCAAGCTAAAGCGATCTCTGT 272
Qy 191 AACGTGACGCCGTGAAGTGTCTGTACGGTTTGGGTGACATCCATGG 250
Db 273 AATGTTCAACCGTTAAGTGTCCGGTTACGGTATCGCGCGATATCCATGG 332
Qy 251 GATCTCATCGAGCTTTCCGCATAGGAGGCAAGCGCCGACACGAACTA 310
Db 333 GACCTAATTGAGCTATTTCGTATTGGTGGTAATGCTCTCTGATCTAATA 392
Qy 311 GCGCACTATGTGGATCGTGGATATATTCTCTCGAGACTGTGTGCTCTT 370
Db 393 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTATT 452
Qy 371 AAGTGGCGGTATAGGATAGGATCAATCTTGGAGGGAACCCAGAGAG 430
Db 453 AAGTGGCGTTACAGGGACAGACTTACGATCTCGAGGGAATCATGAGAG 512
Qy 431 ACGCAAGTATATGTTCTTATGATGAATGCTCGGGAAGTAGGAAATGCG 490
Db 513 ACACAAGTCTATGGTTTTTATGACGAATGCTTGAGGAAATACGGAATGCG 572
Qy 491 AAGTACTTTCAGGATCTGTCTCGACTACCTGCTCTGACAGCTCTCAITG 550
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Qy 551 TTTTGTCTTATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACAT 610
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Qy 611 GATCGTATTCAGAAGTGCCTCCACAGGCGCCGATGTGTGATCTACTCTG 670
Db 693 GATCGAATACAAGAGGTTCCACAGGAAGGACCAATGTGCGATCTACTCTG 752
Qy 671 GATGATCGTTGTGGATGGGCAATTTCAACAGAGTGCCTGTTTACTTTT 730
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Qy 791 GTGATGGAAGGATACAAATTTGGTGCAGGATAAAAATGTTGTACAGTTT 850
Db 873 GTAATGGAGGCTATATTGTTGTGAGGAAAGAACGTAGTGAAGTGT 932
Qy 851 AATTACTGTTTACCGCTGTGGGAACATGGCCGCCATTAATGGAGATAGATGA 910
Db 933 AACTACTGTTTACAGATGTGGAAACATGGCCGCCAAATTTCTTGAGATTGGAGA 992
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Qy 911 CGGTCTTTTCTTCAGTTCGAACGACGCGCGGCAAGTGAACGAGATGTGACGGGAAG 970
Db 993 CAGAACTTCCTTCAATTCCGATCCAGCACCTAGACAGTCCGAACCCGATACCAACGCAAG 1052
Qy 971 ACTCCTGATTACTTTCTGTAA 991
Db 1053 ACCCCTGATTATTTTGTGA 1073

Search completed: December 9, 2005, 08:23:50
Job time : 6828 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 04:43:25 ; Search time 819 Seconds
(without alignments)
11107.821 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggaggag.....tatggcatgctcgagctgc 1365

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1365	100.0	1365	6	ABN81332
2	1365	100.0	1365	8	ABX16239
3	596.6	43.7	1732	13	ADX64434
4	589.6	43.2	1386	10	ACC43349
5	584	42.8	1330	10	ACC43354
6	582.8	42.7	1298	10	ACC43351
7	579.6	42.5	1422	3	AAC46572
8	575.4	42.2	1344	3	AAC44779
9	573.8	42.0	921	3	AAC43084
10	561	41.1	1267	3	AAC40149
11	559.4	41.0	921	3	AAC43368
12	559.4	41.0	921	6	AB212900
13	552.8	40.5	1243	10	ACC43342
14	539.4	39.5	1259	3	AAC45630
15	531.8	39.0	924	6	AB212766
16	531.8	39.0	1110	3	AAC42354
17	525.8	38.5	1484	13	ADT15863
18	517.4	37.9	1487	10	ACC43350
19	515.6	37.8	2574	6	ABT07389

20	515.6	37.8	2574	10	AAD51129	Aad5
21	514	37.7	1279	10	ACC43339	Acc4
22	514	37.7	1522	12	ADQ85030	Adq8
23	514	37.7	1531	10	ADD18470	Add1
24	512.4	37.5	1529	6	ABN95600	Abn9
25	512.4	37.5	1541	10	ADB85530	Adb8
26	512.4	37.5	1541	10	ADC16745	Adc1
27	512.4	37.5	1541	10	AAD51130	Aad5
28	512.4	37.5	1541	14	ADX08186	Adxc
29	512.4	37.5	1541	14	ADX03728	Adxc
30	510.8	37.4	930	6	AB19353	Ab19
31	510.2	37.4	1580	11	ADW22196	Adw2
32	510.2	37.4	1843	6	ABT07396	Abt0
33	510.2	37.4	1843	6	ABK63718	Abk6
34	510.2	37.4	1843	10	ADB58232	Adb5
35	510.2	37.4	1843	10	ABT41939	Abt4
36	510.2	37.4	1843	13	ADV41053	Adv4
37	507.6	37.2	1804	6	ABK63717	Abk6
38	507.6	37.2	1804	10	ADB58231	Adb5
39	507.6	37.2	1804	10	ADB52760	Adb5
40	507.6	37.2	1804	13	ADV41052	Adv4
41	507.6	37.2	1804	14	ADY97843	Adv9
42	506	37.1	1738	11	ADW22195	Adw2
43	506	37.1	1738	12	ADP72938	Adp7
44	505.2	37.0	2181	6	ABV94193	Abv9
45	505.2	37.0	2181	10	ADB85531	Adb8

ALIGNMENTS

RESULT 1

ABN81332

ID ABN81332 standard; cDNA; 1365 BP.

XX

AC ABN81332;

XX

DT 02-SEP-2002 (first entry)

XX

DE Physcomitrella patens PP2A-4 encoding cDNA SEQ ID NO 8.

XX

KW Physcomitrella patens; PHSRP; phosphatase stress related pr

PP2C; enzyme; transgenic; plant; stress tolerance; gene; se

XX

OS Physcomitrella patens.

XX

FH Key Location/Qualifiers

CDS 71..991

FT /*tag= a

FT /product= "PP2A-4"

XX

PN WO200246442-A2.

XX

PD 13-JUN-2002.

XX

PF 06-APR-2001; 2001WO-US011253.

XX

PR 07-APR-2000; 2000US-0196001P.

XX

PA (BADI) BASF PLANT SCI GMBH.

XX

PI Da Costa E Silva, Bohnert HJ, Ishitani M, Van Thienen N

XX

DR WPI; 2002-508562/54.

DR

XX P-FSDB; ABH77578.

PT

New transgenic plant cell transformed by phosphatase stress

protein coding nucleic acid whose expression in the cell re

increased tolerance to environmental stress compared to wil

XX

PS Claim 18; Fig 2; 106pp; English.

XX

CC The invention relates to a transgenic plant cell (I) transf

a

R;

P2A;

ell.

PA (BOHN/) BOHNERT H J.
PA (VTHI/) VAN THIELEN N.
PA (CHEN/) CHEN R.
PA (ISHI/) ISHITANI M.
XX

PI Da Costa E SilvaO, Bohnert HJ, Van Thielen N, Chen R, Ishitani M;
XX
XX
DR WPI; 2003-198392/19.
DR P-PSDB; ABG74203.
XX

XX New transgenic plant cell transformed by a Phosphatase Stress-Related
PT Protein (PHSRP) coding nucleic acid, useful for modifying stress
PT tolerance of a plant.
XX

XX Claim 18; Fig 2C; 79pp; English.
XX

CC The invention relates to a transgenic plant cell transformed by a
CC Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid. The
CC expression of the nucleic acid in the plant cell results in increased
CC tolerance to an environmental stress (e.g. salt tolerance, cold and
CC drought) as compared to a wild type variety of the plant cell. Also
CC include are a transgenic plant comprising the novel plant cell, a seed
CC produced by the transgenic plant of (where the seed is true breeding for
CC an increased tolerance to environmental stress as compared to a wild type
CC variety of the plant cell, an agricultural product produced by the plant
CC or seed, an isolated PHSRP or PHSRP coding nucleic acid, a recombinant
CC expression vector comprising the nucleic acid, and producing a transgenic
CC plant containing PHSRP nucleic acid. The transgenic plant cell
CC transformed by a Phosphatase Stress-Related Protein (PHSRP) coding
CC nucleic acid is useful for modifying stress tolerance of a plant. The
CC present sequence encodes the PHSRP, protein phosphatase, PP2A-4

XX Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Query Match 100.0%; Score 1365; DB 8; Length 1365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGGTTAACCGCGGAGGAGCGGATCGTTAGGTTTGGTCCAGGGGGAGGCGAGA 60

QY 61 GGTGGGCAATCCCGTCTATGCGAGATGACCGCGCAGATGAGACGCTGTCGGAGTG 120
DB 61 GGTGGGCAATCCCGTCTATGCGAGATGACCGCGCAGATGAGACGCTGTCGGAGTG 120

QY 121 CAAGCCGTTGTCGGAGTTCGGAGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGT 180
DB 121 CAAGCCGTTGTCGGAGTTCGGAGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGT 180

QY 181 GGAGGAGTGAACGTCGAGCCGTCGAGTGTCCTGTCACGGTTTCGGTGACATCCATGG 240
DB 181 GGAGGAGTGAACGTCGAGCCGTCGAGTGTCCTGTCACGGTTTCGGTGACATCCATGG 240

QY 241 CCAGTTTCATGATCTCATCGAGCTTTCCGCGATAGGAGCAAGGCGCCGACACGAACTA 300
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QY 301 CTTGTTTCATGGCGGACTATGCGATCGTGATATTTCTGTCGAGACTGTGTCGCTCTT 360
DB 301 CTTGTTTCATGGCGGACTATGCGATCGTGATATTTCTGTCGAGACTGTGTCGCTCTT 360

QY 361 AGTGGCCCTGAAGGTCGGGTATAGGATAGGATCAATCTTGGCGGGAACACGAGAG 420
DB 361 AGTGGCCCTGAAGGTCGGGTATAGGATAGGATCAATCTTGGCGGGAACACGAGAG 420

QY 421 CAGGCGAGATTACGCAAGTATATGGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGC 480
DB 421 CAGGCGAGATTACGCAAGTATATGGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGC 480

QY 481 GAATGTTTGAAGTACTTCACCGGATCTGTTTCGACTCTCTGACAGCTCTCATGGA 540
DB 481 GAATGTTTGAAGTACTTCACCGGATCTGTTTCGACTCTCTGACAGCTCTCATGGA 540

QY 541 GCACGAGATTTTTCGTTCTTTCATGGTGGTCTGTCTCCATCGCTCGACACAT AT 600
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QY 781 TCACGAGTTTGTGATGGAAGGATCAATTTGGTCCAGGATAAAAAATGTTG TT 840
DB 781 TCACGAGTTTGTGATGGAAGGATCAATTTGGTCCAGGATAAAAAATGTTG TT 840

QY 841 CAGTCCCGCCCAATTACTGTTACCGCTGTGGNAACATGGCCGCCATAATGG GA 900
DB 841 CAGTCCCGCCCAATTACTGTTACCGCTGTGGNAACATGGCCGCCATAATGG GA 900

QY 901 AACATGAATCGGTCTTTTCTTTCAGTTTCGAACCGACACCGCGGCAAGTGC GT 960
DB 901 AACATGAATCGGTCTTTTCTTTCAGTTTCGAACCGACACCGCGGCAAGTGC GT 960

QY 961 GACGCGGAAGACTCCTGATTAATTTCTGTAAACATGGGCTATACATGGTA TT 1020
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QY 1021 ACTGAATTTGTTCTGTATAGTCACCTTCCATGGAAGCAGTTTGGCCCTGAA CT 1080
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QY 1081 CCCTCATGATCTAGTAGTATGAAGTTATCTTCTTTGAAAGTGTGTTGTTCCC TA 1140
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QY 1201 CTGCGACAAAGGAGCAGTGTCAATGGTTGCAAGGTTTATAGTGATTAGG GT 1260
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QY 1321 AACGTTTCATCCACACCTACTGTATATGGCATGCTCGAGCTCGC 1365
DB 1321 AACGTTTCATCCACACCTACTGTATATGGCATGCTCGAGCTCGC 1365

RESULT 3
ADX64434

ID ADX64434 standard; cDNA; 1732 BP.

XX ADX64434;

XX 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 35277.

XX plant protectant; plant growth regulant; gene therapy; plan.
KW recombinant DNA construct; physical array; plant breeding n
KW cold tolerance; heat tolerance; drought tolerance; herbicid
KW extreme osmotic condition; pathogen tolerance; pest tolerar
KW growth rate; cell cycle pathway; disease resistance;

nce;

KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.

OS Unidentified.

US2004034888-A1.

PD 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/J) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.

PA (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX Claim 1; SEQ ID NO 35277; 15pp; English.

CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

SQ Sequence 1732 BP; 442 A; 392 C; 457 G; 441 T; 0 U; 0 Other;

Query Match 43.7%; Score 596.6; DB 13; Length 1732;
Best Local Similarity 76.9%; Pred. No. 3.8e-175;
Matches 728; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 48 GGGGGGAGGCGAGAGGTTGGGCAATGCCGTCTATATGAGATGTAGACCGGAGATAGAGC 107
DB 199 GTAGAGCGGAGCGCGAGCGCGATGCCGTGCGACCGGATCTGGACCAACGATCTCGC 258
QY 108 AGCTGTGCGAGTGCAGCGCGTTGTGCGAGTTGGAGTTGAAGAACCTATGTATCAAGCTC 167
DB 259 AGCTGCGGAGTTGCAAGTTCCTGCGCGAGGTGAAGCGTATCGGAGAGGCA 318
QY 168 GGAACATCTTGTGGAGGATGGAAGCTGACCGGTGAAGTGTCTGTACAGTTTCG 227
DB 319 AGGCGATCTCTATGAGGAGTGAAGCTGACCGCGTGCCTGCGCTCACTGTGTGCG 378
QY 228 GTGACATCCATGCCAGTTTTCATGATCTCATGAGCTTTTCGCGCATAGGAGCGAGCGC 287
DB 379 GCGACATCCAGCGCAGTTTCTACGACCTCATGAGCTTTCGCGCATCGCGCGAGCGC 438

QY 288 CCGACACGAACTACTTGTTCATGGCGGCACTATGTGGATCGTGGATATTAT* 3A 347
DB 439 CAGACACCAACTACTCTTTTATGGCGGATTAAGTCGACCGTGGCTACTAC* 3A 498
QY 348 CTGTGTGCTCTTATAGTGGCCCTGAAGGTGCGGTATAGGGATAGGATCACA 4G 407
DB 499 CTGTGTGCTTGTAGTGGCTCTAAAGTACGTTATAGAGACAGATCACA 4G 558
QY 408 GGAACACGAGAGCGAGGAGATTAAGCAAGTATATGGTTTCTATGATGAA* 3A 467
DB 559 GAAATCATGAGAGCAGACAAATAACTCAAGTGTATGGCTTCTATGATGAA* 3A 618
QY 468 AGTATGGAATGCGAATGTTTGGAACTACTTCCGATCTGTTGACACTAC 3A 527
DB 619 AATATGGAATGCAAAATGTGTGGAAGTACTTTTACAGACTTGTGTTGATTAT* 3A 678
QY 528 CAGCTCTCATTTGAGCAGAGATTTTGTCTTTCATGGTGGTCTGTCTCCA* 3A 587
DB 679 CAGCTCTTTATAGAAAACAGATCTTCTGCCATACATGGTGGTCTCTCTCA 3A 738
QY 588 CATTAGATCACATCCGAGCCCTAGATCGTATTCAGAAAGTCCCGCACGAG 3T 647
DB 739 CATTGGATAATATCCGCGCCCTTGATCGCATACAAGAGGTCCCAATGAA* 3T 798
QY 648 GTGATCTACTCTGTCTGATCCAGATGATGTTGTGGATGGGGCATTTTCA* 3G 707
DB 799 GTGATCTTTTGTGGTCTGACCCAGATGACCGATGTGGGTGGGGAATTTCA 3G 858
QY 708 CCGGTATACATTTTGGTCAAGATATTGCGAGAGCAGTTTCAATCATACCAAT 3T 767
DB 859 CTGATACACATTTTGGCCAGATATTGCAACAAATTCACCATCAAAAT* 3C 918
QY 768 TGGTTGACGCTGCTCACCAGCTTGTGATGGAAGATACAATTTGGTGGCCAG 3G 827
DB 919 TTAATTTCAAGGGCACATCAACTTGTATGGAAGGCTTCAATTTGGTGTCA* 3G 978
QY 828 TTGTCACAGTTTTCAGTGGCCCCCAATTAATCTGTACCGCTGTGGGACATG 3A 887
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QY 888 TGGAGATAGATGAACAAATGAATCGTCTTTTCTTCAGTTTCGAAACGACA 3A 947
DB 1039 TCGAAATTTGGCGAGAACATGATCAGAACTTCTTCCAAATTCGACCCAGCT 3A 1098
QY 948 GTGAACACAGATGTGACGCGGAGAGCTCTGTGATTAATTTCTGTAAACA 99.
DB 1099 TTGAGCCGACATGACGCGCAAGACACACAGACTACTTTTGTAGAAA 11.
RESULT 4
ACC43349
ID ACC43349 standard; cDNA; 1386 BP.
XX ACC43349;
XX AC ACC43349;
XX DT 11-AUG-2003 (first entry)
XX DE Protein phosphatase stress-related polypeptide GmPP2A-5 cDN.
XX KW Protein phosphatase stress-related polypeptide; PPSRP; PpPP;
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; 1
XX drought; salinity; cold; enzyme; gene; ss.
OS Glycine max.
XX Key Location/Qualifiers
FH 92.1012
FT /*tag= a
FT /product= "protein phosphatase stress-relat
XX polypeptide"
XX

XX WPI; 2003-300886/29.
DR P-PSDB; ABP98039.
XX
XX New protein phosphatase stress-related polypeptide coding nucleic acid,
PT useful for modulating plant's tolerance to an environmental stress such
PT as drought, increased salinity and cold.
XX
XX Claim 1; Page 87-88; 107pp; English.
XX
XX The present sequence encodes a protein phosphatase stress-related
CC polypeptide (PPSRP). The specification describes PPSRP polypeptides
CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1,
CC GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from
CC Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
CC polypeptides and polynucleotides are useful for modulating plant
CC tolerance to an environmental stress such as drought or increased
CC salinity and cold. They are also useful in identification and
CC localization of Physcomitrella patens, Brassica napus, Glycine max or
CC Oryza sativa and related organisms, mapping of genomes of organisms
CC related to the above species, in a evolutionary and polypeptide
CC structural studies, in determination of PPSRP regions required for
CC function, modulation of PPSRP activity, modulation of metabolism of one
CC or more cell functions and transmembrane transport of one or more
CC components
XX
SQ Sequence 1330 BP; 366 A; 263 C; 327 G; 374 T; 0 U; 0 Other;
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Db |||||
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Db |||||
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Qy |||||
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AC ACC43351;
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DT 11-AUG-2003 (first entry)
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DE Protein phosphatase stress-related polypeptide OsPP2A-2 cDN.
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KW Protein phosphatase stress-related polypeptide; PPSRP; PpPP
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; j
KW drought; salinity; cold; enzyme; gene; ss.
OS Oryza sativa.
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FT CDS /*tag= a
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PD 13-MAR-2003.
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PF 05-SEP-2002; 2002WO-US028445.
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PP 05-SEP-2001; 2001US-0317305P.
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PI Bohnert HU, Chen R, Ishitani M, Van Thielien N, Da Costa
XX WPI; 2003-300886/29.
DR P-PSDB; ABP98036.
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XX New protein phosphatase stress-related polypeptide coding m
PT useful for modulating plant's tolerance to an environmental
PT as drought, increased salinity and cold.
XX
PS Claim 1; Page 84; 107pp; English.
XX
CC The present sequence encodes a protein phosphatase stress-r-
CC polypeptide (PPSRP). The specification describes PPSRP poly
CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, (
CC GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
CC Physcomitrella patens, Brassica napus, Glycine max or Oryza
PPSRP

Qy	97	GCAGATAGAGCAGCTGTGCGGAGTGCAGACCGTGTTCGAGGTTCGAGGTGAAGAACCTATG	156
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Qy	157	TGATCAAGACTCGGACGATCTTGGTGGAGGAGTGCNAACGTGCAGCCCGTGAAGTGTCTCTGT	216
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ID AAC44779 standard; DNA; 1344 BP.
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AC AAC44779;
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DT 18-OCT-2000 (first entry)

XX	Zea mays DNA fragment SEQ ID NO: 44101.
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XX	Hybridisation assay; genetic mapping; gene expression contr
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PR 29-OCT-1999; 99US-0162142P.

Query Match 42.2%; Score 575.4; DB 3; Length 13.
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Matches 717; Conservative 0; Mismatches 236; Indels

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DB 203 CGGCGGGAGCGGCGCGGACGAGATGCCGTCCACGGGATCTGGAC;
QY 105 AGCAGCTGTCGGAGTGAAGCGGTTGTTCGGAGTTGGAGGTGAAGAACCTTA'
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PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
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XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27232.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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Db 1059 ACCCTGATTATTTTGTGA 1079

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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 39005.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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PN EP1033405-A2.
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Best Local Similarity 75.5%; Pred. No. 1.2e-163;
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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QY	311	GGCGACTATGCGATCGTGATATATTCTCTCGAGACTGTGTCTGCTCTT
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Db	661	ATTGCTACTCAGTTTAAATCATAAACAATGGACTGAGTCTGATCTCAAGAGC
QY	791	GTGATGGAGGATACAAATGTGTGCGAGGATAAAATGTTGTTCACAGTTTT
Db	721	GTAATGGAAAGCTATAATTGGTGTGAGGAAAGAACGTAAGTACAGTGT
QY	851	AATTACTGTTACCGCTGTGGGAACATGGCCGCCATAATGGAGATAGATGA
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QY	911	CGGTCTTTTCTTCAGTTCGAACCGACACCGCGGCAAAAGTGAACCGAGATG
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QY	971	ACTCCTGATTACTTCTGTAA 991
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RESULT 12
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XX	AC	ABZ12900;
XX	DT	21-JAN-2003 (first entry)
XX	DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 705.
XX	KW	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX	OS	Arabidopsis thaliana.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 06:03:11 ; Search time 5144 Seconds
(without alignments)
12415.313 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcgaggag.....tatggcatgctcgagctgc 1365

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
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- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_gss1:*
- 10: gb_gss2:*
- 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	738.4	54.1	740	3	BJ598448
C 3	736.8	54.0	752	3	BJ591074
C 4	734.8	53.8	762	3	BJ976562
C 5	697.8	51.1	706	3	BJ585338
C 6	680.4	49.8	706	3	BJ599008
C 7	653	47.8	666	3	BJ503182
C 8	576.2	42.2	1429	4	AY104802
C 9	574.2	42.2	921	10	CL964875
C 10	574.2	42.1	1283	4	CNS0ADRX
C 11	571	41.8	1285	4	CNS0AD99
C 12	564.6	41.4	1278	4	CNS0ADNP
C 13	556.6	40.8	1534	4	AY108657
C 14	556.2	40.7	1250	4	CNS0ADL7
C 15	520.2	38.1	849	7	CO082158
C 16	516.6	37.8	1586	4	AY609732
C 17	515.6	37.8	1723	4	CR624064
C 18	513.8	37.6	933	7	CV291986
C 19	507.8	37.2	906	7	CK278240
C 20	504.8	37.0	797	8	DR683092
C 21	504.2	36.9	1371	4	CNS0A3F1
C 22	503.6	36.9	1749	4	CR594899

23	503.6	36.9	1758	4	CR624778
24	503.6	36.9	1781	4	CR596427
25	503.6	36.9	1830	4	CR619537
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32	492	36.0	870	5	BU133847
33	491.8	36.0	763	1	AJ080257
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36	486.2	35.6	1430	4	CR611096
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39	483.2	35.4	945	6	CF584336
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43	477.6	35.0	1770	4	CNS0FR02
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ALIGNMENTS

RESULT 1
BJ587709/c

LOCUS

DEFINITION

BJ587709 normalized full length cDNA library, linear
caulonemata and malformed buds Physcomitrella patens
cDNA clone pbhb34c10 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

T-2003

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on

(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCObase (<http://moss.nibb.ac.jp/>).

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RESULT 2
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LOCUS

DEFINITION

Location/Qualifiers

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/db_xref="taxon:145481"

/clone="pphb34c10"

/tissue_type="mixture of chloronemata, caulonemata and

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chloronemata, caulonemata and malformed buds"

ORIGIN

Query Match

Best Local Similarity

Matches 739; Conservative

0; Mismatches 1; Indels

0;

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Db 680 GTTGTGGATGGGTATTTTACCACGAGGTCCGCGTTATCTTTTGGTCAA

BU598448

740 bp mRNA linear

BU598448 normalized full length cDNA library, chloro

caulonemata and rhizoid-like protonemata Physcomitre

subsp. patens cDNA clone pphn23h10 3', mRNA sequence

BU598448

GI:37840440

EST.

Physcomitrella patens subsp. patens

Physcomitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Bryopsida; Funariidae; Funariales; Funariaceae; Phys.

1 (bases 1 to 740)

Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide

Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y.,

Kohara,Y. and Hasebe,M.

Comparative genomics of Physcomitrella patens gameto

transcriptome and Arabidopsis thaliana: implication

evolution

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2

12808149

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescri

that was in vivo excised from a l-FLC phage vector (

2001). 5' end of the cDNA that was digested with Xho

to SalI site of the vector and the 3' end including

ligated to BamHI site of the

vector(5'- GAGAGAGAGGATCCAAACCCCTGGAGAGTTTTTTTTTTT

used as a 1st 3' primer, and

5'-ggTCTCGATCgTgTTCAGACAGCGATgACTCGAGAACCGNNN

5'-hairpin primer, giving the following 5' boarder s

AGCCAAATCGCGAGCTCGAATTCGTGGAACCG). cDNA insert

amplified with conventional T7 and T3 primers. This

cDNA library was generated according to the method d

Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then c

the BCDAT medium for 13- 14 days under the continuo

These clones are available from RIKEN Bio Resource C

(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>).

of Physcomitrella EST clones is available at the PHY

(<http://moss.nibb.ac.jp/>).

Location/Qualifiers

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/tissue_type="mixture of chloronemata, caul

rhizoid-like protonemata"

/clone_lib="normalized full length cDNA lib

chloronemata, caulonemata and rhizoid-like ;

ORIGIN

Query Match

Best Local Similarity

Matches 739; Conservative

0; Mismatches 1; Indels

0;

QY 618 TTCAGAGTGTCCCGACGAGGCCCGATGTGTGATCTACTCTGGTCTGAT

Db 740 TTCAGAGTGTCCCGACGAGGCCCGATGTGTGATCTACTCTGGTCTGAT

QY 678 GTTGTGGATGGGCATTTTACCACGAGGTCCGCGTTATCTTTTGGTCAA

Db 680 GTTGTGGATGGGTATTTTACCACGAGGTCCGCGTTATCTTTTGGTCAA

FEATURES

source

1..746

/organism="Physcomitrella patens subsp. patens"

/mol_type="mRNA"

/sub_species="patens"

/db_xref="taxon:145481"

/clone="pphb34c10"

/tissue_type="mixture of chloronemata, caulonemata and

malformed buds"

/clone_lib="normalized full length cDNA library,

chloronemata, caulonemata and malformed buds"

ORIGIN

Query Match

Best Local Similarity

Matches 742; Conservative

0; Mismatches 1; Indels

0; Gaps

0;

QY 615 GTATTCAAGAGTGC CGCACGAGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATG 674

Db 746 GTATTCAAGAGTGC CGCACGAGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATG 687

QY 675 ATCGTTGTGGATGGGCGATTTTCCACACAGAGTGGCGGTATATCTTTTGGTCAAGATATTG 734

Db 686 ATCGTTGTGGATGGGCGATTTTCCACACAGAGTGGCGGTATATCTTTTGGTCAAGATATTG 627

QY 735 CAGACAGTTCATATACATACCAATGCTCTAAAGTTTGGTTCGACGTCTCCACAGCTTTGTA 794

Db 626 CAGACAGTTCATATACCAATGCTCTAAAGTTTGGTTCGACGTCTCCACAGCTTTGTA 567

QY 795 TGGAAAGATACAATTGGTCCAGGATAAAAATTTGTTCACAGTTTTCAGTGCCGCCCAATT 854

Db 566 TGGAAAGATACAATTGGTCCAGGATAAAAATTTGTTCACAGTTTTCAGTGCCGCCCAATT 507

QY 855 ACTGTTACCGCTGTGGACATATGCGCGCCATATGAGATAGATGAACAATGAATCGGT 914

Db 506 ACTGTTACCGCTGTGGACATATGCGCGCCATATGAGATAGATGAACAATGAATCGGT 447

QY 915 CTTTTCCTTCAGTTCGAACACAGCACCGCGCAAGTGAACAGATGTGACGGGAAGACTC 974

Db 446 CTTTTCCTTCAGTTCGAACACAGCACCGCGCAAGTGAACAGATGTGACGGGAAGACTC 387

QY 975 CTGATTACTTTCTGTAACATGGCCCTATACATGTFACCTTTTACTTACTGAATTTGTTCTG 1034

Db 386 CTGATTACTTTCTGTAACATGGCCCTATACATGTFACCTTTTACTTACTGAATTTGTTCTG 327

QY 1035 TATAGTCACCTTCATGGAAGCAGTTTGGCCCTGAATGAAGATATCTCCCTCATGATCTAG 1094

Db 326 TATAGTCACCTTCATGGAAGCAGTTTGGCCCTGAATGAAGATATCTCCCTCATGATCTAG 267

QY 1095 TAGTATGAAGTTATCTCTCTTTGAAGTGTGTGTTCCCTTTTGTAGTACTTGCTCCTCTGTT 1154

Db 266 TAGTATGAAGTTATCTCTCTTTGAAGTGTGTGTTCCCTTTTGTAGTACTTGCTCCTCTGTT 207

QY 1155 CATTTCATAAAGTTGCTTCAGAACCAACTGAGATGTTGTAATGTAACTGCGCAAGAGGA 1214

Db 206 CATTTCATAAAGTTGCTTCAGAACCAACTGAGATGTTGTAATGTAACTGCGCAAGAGGA 147

QY 1215 GCAGTGTCAATGGTTGCAAGGGTTATAGTATAGGGAAGAGGTAGCATGTTACTT 1274

Db 146 GCAGTGTCAATGGTTGCAAGGGTTATAGTATAGGGAAGAGGTAGCATGTTACTT 87

QY 1275 CAAATCGATCAGAGACTTCTATGGAAGATGACGATGGTGAACCAACAGTTTCATCTCCA 1334

Db 86 CAAATCGATCAGAGACTTCTATGGAAGATGACGATGGTGAACCAACAGTTTCATCTCCA 27

QY 1335 CACCTACTGTATATGGCATGCTC 1357

Db 26 CACCTACTGTATATGGCATGCTC 4

738	QY	AGCAGTTCAATCATACCAATGGTCTAAAGTTTGGTTGCAACGCTGCTCACAGCTGTGTGAAG	797
620	Db	AGCAGTTCAATCATACCAATGGTCTAAAGTTTGGTTGCAACGCTGCTCACAGCTGTGTGAAG	561
798	QY	AAGGATACAATTGGTGTCCAGGATAAAATGTTGTACAGTTTTTCAGTGGCCCCCAATTACT	857
560	Db	AAGGATACAATTGGTGTCCAGGATAAAATGTTGTACAGTTTTTCAGTGGCCCCCAATTACT	501
858	QY	GTTTACCCTGTGGGAACATGCGGCCCATATAATGGAGATAGATGAATAAATGAATCGGTCCT	917
500	Db	GTTTACCCTGTGGGAACATGCGGCCCATATAATGGAGATAGATGAATAAATGAATCGGTCCT	441
918	QY	TTCTTTCAAGTTTCGAACACAGCACCGCGGCAAAAGTGAACCCAGATGTGACGCGGAAGACTCCTG	977
440	Db	TTCTTTCAAGTTTCGAACACAGCACCGCGGCAAAAGTGAACCCAGATGTGACGCGGAAGACTCCTG	381
978	QY	ATTACTTTCTGTAACATGCGCCTATACATGGTACTCTTTTACTTACTGAAATGTTCTGTAT	1037
380	Db	ATTACTTTCTGTAACATGCGCCTATACATGGTACTCTTTTACTTACTGAAATGTTCTGTAT	321
1038	QY	AGTCACCTTCATGGAAGCAGTTTGGCCCTGGAATGAAGATGACTCCCTCATGATCTAGTAG	1097
320	Db	AGTCACCTTCATGGAAGCAGTTTGGCCCTGGAATGAAGATGACTCCCTCATGATCTAGTAG	261
1098	QY	TATGAAGTTATCTTTTGAAGTGTGTTGTTCCCTTTTTTATAGTACTTGCTCCTCTGTTTCAT	1157
260	Db	TATGAAGTTATCTTTTGAAGTGTGTTGTTCCCTTTTTTATAGTACTTGCTCCTCTGTTTCAT	201
1158	QY	TCATAAAGTTGCCCTTCAGAACAACTGAGATGTTGTGAATGTAACTGCGACAAGAGGAGCA	1217
200	Db	TCATAAAGTTGCCCTTCAGAACAACTGAGATGTTGTGAATGTAACTGCGACAAGAGGAGCA	141
1218	QY	GTGTCAATGGTTGCAAGGGTTATAGTGATTTAGGGAAGAAGGTAGACATGTTACTTCAA	1277
140	Db	GTGTCAATGGTTGCAAGGGTTATAGTGATTTAGGGAAGAAGGTAGACATGTTACTTCAA	81
1278	QY	ATCGATCAGAGACTTCTATCGAAAAAGATGACGATGGTGGAAAAACAACCTTCATCTCCACAC	1337
80	Db	ATCGATCAGAGACTTCTATCGAAAAAGATGACGATGGTGGAAAAACAACCTTCATCTCCACAC	21
1338	QY	CTACTGTATATGGCATGCTC	1357
20	Db	CTACTGTATATGGCATGCTC	1

RESULT		3
BJ591074/c		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL:		
PUBLISHED		
COMMENT		

EST 22-OCT-2003

BJ591074 mRNA linear
 BJ591074 normalized full length cDNA library, chloronata, patens caulonemata and malformed buds Physcomitrella patens subsp. patens cDNA clone ppbb42k24 3', mRNA sequence.

BJ591074
 BJ591074.1 GI:37833062 EST.
Physcomitrella patens subsp. *patens*
Physcomitrella patens subsp. *patens*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariales; *Physcomitrella*.
 1 (bases 1 to 752)
 Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe.M.
 Comparative genomics of *Physcomitrella patens gametophytic transcriptome* and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)

12808149
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute Of Genetics
 1111 Yatae, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript⁺ that was in vivo excised from a 1-FLC phage vector (2001). 5' end of the cDNA that was digested with XbaI to SalI site of the vector and the 3' end including ligated to BamHI site of the vector (5'- gagAGAGAGAGATCCACCTCGgAgGATTTTTTTTTTTT vector (5'- gagAGAGAGAGATCCACCTCGgAgGATTTTTTTTTTTT used as a 1st 3' primer, and 5'-ggTTCGAGTCACTGCTTCCAGACAGCgATgACTCGAGAACCGNN 5'-hairpin primer, giving the following 5' boarder AGCCAAATCGCGAGCTCGAATCGTCGAGAACCG). cDNA instert amplified with conventional 17 and T3 primers. This cDNA library was generated according to the method of Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then the BODATG medium for 13- 14 days under the continu These clones are available from RIKEN Bio Resource (http://www.brc.riken.go.jp/lab/epd/Eng/index.html) of Physcomitrella EST clones is available at the PHY (http://moss.nibb.ac.jp).

Location/Qualifiers

1. 752

/organism="Physcomitrella patens subsp. pat

/mol_type="mRNA"

/sub_species="patens"

/db_xref="taxon:145481"

/clone="pphb42k24"

/tissue_type="mixture of chloronemata, caul

malformed buds"

/clone.lib="normalized full length cDNA lib

chloronemata, caulonemata and malformed bud

ORIGIN

	Query Match	54.0%; Score 736.8; DB 3; Length 75
	Best Local Similarity	99.1%; Pred. No. 9.1e-207;
	Matches	741; Conservative 0; Mismatches 7; Indels
Qy	618	TTCAAGAGTGC CGCAGAGGCGCGATGTGTACTCTGTCGTGAT
Db	752	TTCAAGAGTGC CGCAGAGGCGCGATGTGTACTCTGTCGTGAT
Qy	678	GTGTGTGATGGG CATTTCCACAGAGTGC CGGTATAC TTTTGGTCA
Db	692	GTGTGTGATGGG ATTTTCCACAGAGTGC CGGTATAC TTTTGGTCA
Qy	738	AGCAGTTCAATCATACCAATGGTCTAAGTTGGTTGTCACGTGCTCACCG
Db	632	AGCAGTTCAATCATACCAATGGTCTAAGTTGGTTGTCACGTGCTCACCG
Qy	798	AAGGATACAATTTGGTGC CAGGATAAAAATGTTGTGCACAGTTTTCAGTGCC
Db	572	AAGGATACAATTTGGTGC CAGGATAAAAATGTTGTGCACAGTTTTCAGTGCC
Qy	858	GTTCACCGCTGTGGGAA CATGCGCCCATATGAGAGATAGATGAAACAATG
Db	512	GTTCACCGCTGTGGGAA CATGCGCCCATATGAGAGATAGATGAAACAATG
Qy	918	TTCTTCAGTTTCGAA CCGAGCCGCGGCAAAAGTGAAACAGATGTGACCGCG
Db	452	TTCTTCAGTTTCGAA CCGAGCCGCGGCAAAAGTGAAACAGATGTGACCGCG
Qy	978	ATTACTTTCTGTAAACATGCGCTATACATGGTACTCTTTACTTACTGAA
Db	392	ATTACTTTCTGTAAACATGCGCTATACATGGTACTCTTTACTTACTGAA
Qy	1038	AGTCACCTTCATGGAAGCAGTTTGCCCTCGAATGAAGATACTCCCTCA
Db	332	AGTCACCTTCATGGAAGCAGTTTGCCCTCGAATGAAGATACTCCCTCA
Qy	1098	TATGAAGTTATCTTTTGAAGTGTGTTGTCCTCTTTTATGACTTGCT
Db	272	TATGAAGTTATCTTTTGAAGTGTGTTGTCCTCTTTTATGACTTGCT

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QY 1158 TCATAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAACCTGCCAAGAAGAGGACCA 1217
Db 212 TCATAAAGTTGCCCTTCAGAACAACTGAGATGTTGTGAATGTAACCTGCCAAGAAGAGGACCA 153
QY 1218 GTGTCAATGGTTGCAAGGTTTATAGTGAATAGGGAAGAAGTAGACATGTTACTTCAA 1277
Db 152 GTGTCAATGGTTGCAAGGTTTATAGTGAATAGGGAAGAAGTAGACATGTTACTTCAA 93
QY 1278 ATCGATCAGACATCTTATGGAAGAGATGACGATGGTGAACAAACAGTTCTATCTCCACAC 1337
Db 92 ATCGATCAGACATCTTATGGAAGAGATGACGATGGTGAACAAACAGTTCTATCTCCACAC 33
QY 1338 CTACTGTATATGGCATGCTCGAGCTGC 1365
Db 32 CTACTGTATATGGCATGCTCTTGAGAGC 5

RESULT 4
BJ976562/c
LOCUS BJ976562 ppssp full-length cDNA library Physcomitrella patens subsp.
DEFINITION patens cDNA clone ppssp34i06 3', mRNA sequence.
ACCESSION BJ976562
VERSION BJ976562.1 GI:67726303
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 762)
Nishiyama,T., Fujita,T., Sakakibara,K., Shin-i,T., Kohara,Y. and
Hasebe,M.
Physcomitrella patens EST from young sporophytes with surrounding
archegonia
JOURNAL Unpublished (2005)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp
Mosses were grown for 1-1.5 months at 25C under continuous light
followed for 3-4 weeks at 15C under short-day conditions (8L16D).
Tiny sporophytes with surrounding archegonia were dissected under
stereomicroscope and their RNA was extracted for constructing a
full-length cDNA library. The database of the EST clones is
available at the PHYSCobase (http://moss.nibb.ac.jp).

FEATURES
source
1..762
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
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/tissue_type="sporophytes (embryos) with surrounding
archegonia"
/dev_stages="young sporophytes cultivated for 3-4 weeks at
15C under short-day conditions"
/clone_lib="ppssp full-length cDNA library"

ORIGIN
Query Match 53.8%; Score 734.8; DB 3; Length 762;
Best Local Similarity 99.3%; Pred. No. 3.6e-206;
Matches 758; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 574 TCCATCGCTCCGACACATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAGTCCCGCA 633
Db 762 TCCATCGCTCCGACACATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAGTCCCGCA 703
QY 634 CGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGGGCAT 693
Db 702 CGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGGGTAT 643

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QY 694 TTCACCAAGAGTCCCGTTATATCTTTTGGTCAAGATATTTCAGAGCAGT 753
Db 642 TTCACCAAGAGTCCCGTTATATCTTTTGGTCAAGATATTTCAGAGCAGT 583
QY 754 CAATGGTCTAAGTTTGGTTCACGCTGCTCACCGCTGTGTGATGGAAGAT 813
Db 582 CAATGGTCTAAGTTTGGTTCGCTGCTCACCGCTGTGTGATGGAAGAT 523
QY 814 CCAGGATAAAATCTTGTACAGTTTTTCAAGTCCCAATTTACTGTTTACC 873
Db 522 CCAGGAT-AAAATGTTGTACAGTTTTTCAAGTCCCAATTTACTGTTACC 464
QY 874 CATGGCCGCATATATGGAGATAGATAAACAATGAATCGGTCCTTTCTTC 933
Db 463 CATGGCCGCATATATGGAGATAGATAAACAATGAATCGGTCCTTTCTTC 404
QY 934 AGCACCGCGCAAGTGAACCAAGATGTGACGCGAAGACTCCTGATTACT 993
Db 403 AGCACCGCGCAAGTGAACCAAGATGTGACGCGAAGACTCCTGATTACT 344
QY 994 ATGCGCTATACATCGTACCTTTTACTTACTGAAATGTTTCTGTATAGTCAC 1053
Db 343 ATGCGCTATACATCGTACCTTTTACTTACTGAAATGTTTCTGTATAGTCAC 284
QY 1054 AGCAGTTGGCCCTGAATGAAGATGACTCCCTCATGATCTAGTAGTAGAA 1113
Db 283 AGCAGTTGGCCCTGAATGAAGATGACTCCCTCATGATCTAGTAGTAGAA 224
QY 1114 TTGAAGTGTGTTGTTCCCTTTTATAGTACTTCTCTCTGTTCAATTCATAA 1173
Db 223 TTGAAGTGTGTTGTTCCCTTTTATAGTACTTCTCTCTGTTCAATTCATAA 164
QY 1174 AGAACAACTGAGATGTTGTGAATGTAACCTGCGAACAAGAGGAGCAGTGTC 1233
Db 163 AGAACAACTGAGATGTTGTGAATGTAACCTGCGAACAAGAGGAGCAGTGTC 104
QY 1234 GGGTTATAGTAGTTAGGGAAGAAGAGTAGACATGTTACTTCAATCGAT 1293
Db 103 GGGTTATAGTAGTTAGGGAAGAAGAGTAGACATGTTACTTCAATCGAT 44
QY 1294 TATGGAAGAAGATGA-CGATGTTGGAACAACAGTTCATCTCCAC 1335
Db 43 TATGGAAGAAGATGAATGATGTTGGAACAACAGTTCATCTCCAC 1

RESULT 5
BJ585338/c
LOCUS BJ585338
DEFINITION BJ585338 normalized full length cDNA library, chloro-
caulonemata and malformed buds Physcomitrella patens
cDNA clone pphb27b14 3', mRNA sequence.
ACCESSION BJ585338
VERSION BJ585338.1 GI:37827326
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Phys-
1 (bases 1 to 706)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophyte
transcriptome and Arabidopsis thaliana: implication
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
JOURNAL 12808149
PUBMED Contact: Tadasu Shin-i
COMMENT Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

```

Fax: 81-559-81-6855
Email: tshnigenes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'- GAGAGAGAGAGGATCCCAACCTCGAGAGTGTGTTTATTTTNN-3' was used as a 1st 3' primer, and 5'-GGTCTCGAGTCATCGTGTTCACAGACGATCTCGAGACCGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCGAATCGCGAGTCGATCGAATCTCGAGAACCG). cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
Pronemata were cloned by the POLYTOM, and then cultivated on the BCDATG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCoBase (<http://mosas.nibb.ac.jp/>).

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FEATURES
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malformed buds"
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chloronemata and malformed buds"
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ORIGIN

Query Match	51.1%	Score 697.8	DB 3	Length 706
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Matches 699	Conservative 0	Mismatches 3	Indels 0	Gaps 0
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Db	706	ATTCAAGAACTGCCGACAGAGGCCCATGTGTGATCTACTCTGGTCTGATCCAGATGAT	647	
QY	677	CGTTGTGGATGGGGCATTTACACACAGAGTGCCGGTTTATACTTTTGGTCAAGATATTGCA	736	
Db	646	CGTTGTGGATGGGGTATTTACACAGAGTGCCGGTTTATACTTTTGGTCAAGATATTGCA	587	
QY	737	GAGCAGTTCAATCATACCAATGFTCTAAGTTTGGTTGCACGTGCTCAACAGCTTTGTGATG	796	
Db	586	GAGCAGTTCAATCATACCAATGFTCTAAGTTTGGTTGCACGTGCTCAACAGCTTTGTGATG	527	
QY	797	GAAGGATACAAATTGGTGCCAGGATAAAAATGTTGTCTACAGTTTTTCAGTGCCCCCAATTAC	856	
Db	526	GAAGGATACAAATTGGTGCCAGGATAAAAATGTTGTCTACAGTTTTTCAGTGCCCCCAATTAC	467	
QY	857	TGTTACCGCTGTGGGAACATGGCCGCCATTAATGGAGATAGATGAACAATGAATCGGTCT	916	
Db	466	TGTTACCGCTGTGGGAACATGGCCGCCATTAATGGAGATAGATGAACAATGAATCGGTCT	407	
QY	917	TTTCTTCAGTTCGAACCCAGCACCGCGGCAAGTGAACCCAGATGTGACGCGGAAGACTCCT	976	
Db	406	TTTCTTCAGTTCGAACCCAGCACCGCGGCAAGTGAACCCAGATGTGACGCGGAAGACTCCT	347	
QY	977	GATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTTACTGAATTGTTCTGTA	1036	
Db	346	GATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTTACTGAATTGTTCTGTA	287	
QY	1037	TAGTCACCTTCCATGGAAGCAGTTTGCCCTCGAATGAAGATACTCCCTCATGACTAGTA	1096	
Db	286	TAGTCACCTTCCATGGAAGCAGTTTGCCCTCGAATGAAGATACTCCCTCATGACTAGTA	227	
QY	1097	GTATGAAGTTATCTTCTTTGAAGTTTGTTCCTTTTTTAGTACTTGTCTCTGTTCCTCA	1156	
Db	226	GTATGAAGTTATCTTCTTTGAAGTTTGTTCCTTTTTTAGTACTTGTCTCTGTTCCTCA	167	

[illegible]

ORIGIN

Query Match 49.8%; Score 680.4; DB 3; Length 706;
Best Local Similarity 99.0%; Pred. No. 4.9e-190;
Matches 695; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 665 GATCAGATGATCGTTGGATGGGCAATTCACACAGAGTCGCGGTATATCTTTTGGT 724
Db 706 GATCAGATGATCGTTGGATGGGCAATTCACACAGAGTCGCGGTATATCTTTTGGT 647
QY 725 CAAGATATTGAGAGCAGTTCATATACATACCAATGGTCTAAAGTTGGTTGACGTGCTCAC 784
Db 646 CAAGATATTGAGAGCAGTTCATATACATACCAATGGTCTAAAGTTGGTTGACGTGCTCAC 587
QY 785 CAGCTTGTGATGGAAGAGATACAATTTGGTCAGGATAAAAAATGTTGTACAGTTTTCAGT 844
Db 586 CAGCTTGTGATGGAAGAGATACAATTTGGTCAGGATAAAAAATGTTGTACAGTTTTCAGT 527
QY 845 GCCCCCAATTACTGTTACCGCTGTGGGAACATGGCCGCCATAAATGGAGATAGTAACA 904
Db 526 GCCCCCAATTACTGTTACCGCTGTGGGAACATGGCCGCCATAAATGGAGATAGTAACA 467
QY 905 ATGAATCGGTCTTTCTTCAGTTCGAACACAGCAGCCGCGCAAA-GTGAACACAGATGTGAC 963
Db 466 ATGAATCGGTCTTTCTTCAGTTCGAACACAGCAGCCGCGCAAAANGTGAACAGATGTGAC 407
QY 964 GCGGAAGACTCCTGATTAATCTTCTGTAACAATGCGCTATATACATGATCTTTTACTTACT 1023
Db 406 GCGGAAGACTCCTGATTAATCTTCTGTAACAATGCGCTATATACATGATCTTTTACTTACT 347
QY 1024 GAATTTGTTCTGTATAGTCACCTTCATCGAAGCAGTTTGGCCCTCAATGAAGATACCTCC 1083
Db 346 GAATTTGTTCTGTATAGTCACCTTCATCGAAGCAGTTTGGCCCTCAATGAAGATACCTCC 287
QY 1084 TCATGATCTAGTATGATGAAGTATCTTCTTTGAAGTGTGTTGTTCCCTTTTGTAGTACTT 1143
Db 286 TCATGATCTAGTATGATGAAGTATCTTCTTTGAAGTGTGTTGTTCCCTTTTGTAGTACTT 227
QY 1144 GCTCCTCTGTTCAATTCATTAAGTTGCCCTTCAGAACCACTGAGATGTTGTGAATGTAAC 1203
Db 236 GCTCCTCTGTTCAATTCATTAAGTTGCCCTTCAGAACCACTGAGATGTTGTGAATGTAAC 167
QY 1204 CGACAGAGGAGCAGTGTCAATGGTTGCAAGGTTATAGTATTAGGCAAGAGGTAGC 1263
Db 166 CGACAGAGGAGCAGTGTCAATGGTTGCAAGGTTATAGTATTAGGCAAGAGGTAGC 107
QY 1264 ACATGTTACTTCAAAATCGATCAGAGACTTCTATGAAAAAGATGACATGGTGGAAACAAC 1323
Db 106 ACATGTTACTTCAAAATCGATCAGAGACTTCTATGAAAAAGATGACATGGTGGAAACAAC 47
QY 1324 GTTCATCTCCACCTACTGTATATGCGATGCTCAGCTCGC 1365
Db 46 GTTCATCTCCACCTACTGTATATGCGATGCTCTTGAGAGC 5

RESULT 7
BU603182/c
LOCUS
DEFINITION
BU603182 666 bp mRNA linear EST 22-OCT-2003
BU603182 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphnlp05 3', mRNA sequence.
ACCESSION
BU603182.1 GI:37845174
VERSION
KEYWORDS
SOURCE
ORGANISM
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
1. (bases 1 to 666)
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohara, Y. and Hasebe, M.
Comparative Genomics of Physcomitrella patens gametophytic

transcriptome and Arabidopsis thaliana: implication
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2
12808149
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescri
that was in vivo excised from a l-PUC phage vector (C
2001). 5' end of the cDNA that was digested with Xho
to SalI site of the vector and the 3' end including
ligated to BamHI site of the
vector (5'- gagagagagagatccaaacccctggagagatTTTTTTTTTT
used as a 1st 3' primer, and
5'-gggtctcgatcgatcgctgtccagacagcagatcgactcgagAACCCNNN
5'-hairpin primer, giving the following 5' boarder s
AGCCAAATCGCCGAGCTCGAATCGTCGAGAACCG). cDNA insert
amplified with conventional T7 and T3 primers. This
cDNA library was generated according to the method d
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then c
the BCDATG medium for 13- 14 days under the continuo
These clones are available from RIKEN Bio Resource C
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html).
of Physcomitrella EST clones is available at the PHY:
(http://moss.nibb.ac.jp).

FEATURES

Location/Qualifiers
source 1..666
/organism="Physcomitrella patens subsp. pat.
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphnlp05"
/tissue_type="mixture of chloronemata, caul-
rhizoid-like protonemata"
/clone_lib="normalized full length cDNA lib
chloronemata, caulonemata and rhizoid-like ;

ORIGIN

Query Match 47.8%; Score 653; DB 3; Length 666;
Best Local Similarity 99.2%; Pred. No. 6.5e-182;
Matches 656; Conservative 0; Mismatches 5; Indels 0;
QY 705 GTGCCGGTTTATCTTTTGGTCAAGATATTGCAGAGCAGTTCATCATATACC. A 764
Db 666 GTGCCGGTTTATCTTTTGGTCAAGATATTGCAGAGCAGTTCATCATATACC. A 607
QY 765 GTTTGGTTGACGTGCTCACACAGCTTGTGATGGAAGGATACAATTGGTGC. A 824
Db 606 GTTTGGTTGACGTGCTCACACAGCTTGTGATGGAAGGATACAATTGGTGC. A 547
QY 825 ATGTTGTACAGTTTTCAGTGCCTCCCAATTTACTCTTACCGCTGTGGGAC. A 884
Db 546 ATGTTGTACAGTTTTCAGTGCCTCCCAATTTACTGTATCCGCTGTGGGAC. A 487
QY 885 TAATGGAGATAGATGAACCAATGAATCGGTCTTTTCTTCAGTTTCGAACCA. C 944
Db 486 TAATGGAGATAGATGAACCAATGAATCGGTCTTTTCTTCAGTTTCGAACCA. C 427
QY 945 AAAGTGAACAGATGTGACGCGGAAGACTCCTGATTTACTTTCTGTAAACA. C 1004
Db 426 AAAGTGAACAGATGTGACGCGGAAGACTCCTGATTTACTTTCTGTAAACA. C 367
QY 1005 ATGTTACTTTTACTTACTGAAATGTTCTGTATAGTACACCTTCCATGGAA. C 1064
Db 366 ATGTTACTTTTACTTACTGAAATGTTCTGTATAGTACACCTTCCATGGAA. C 307
QY 1065 CCTGAATGAAGATACCTCCCTCATCATCTAGTATGAGTATGAAGTTATCTTCTT. T 1124

Db 306 CCTGAATGAAGTACTCCCTCATGATCTAGTAGTATGAAGTATCTCTTTCAAGTGT 247

Qy 1125 GTTCCCTTTTGTAGTACTGCTCTCTGTTCAATTCATAAAGTTGCTTCAGAACACTGA 1184

Db 246 GTTCCCTTTTGTAGTACTGCTCTCTGTTCAATTCATAAAGTTGCTTCAGAACACTGA 187

Qy 1185 GATGTTGTAATGTAACTGCGCAAGAGGAGGAGTGTCAATGGTTGCAAGGGTTATAGTG 1244

Db 186 GATGTTGTAATGTAACTGCGCAAGAGGAGGAGTGTCAATGGTTGCAAGGGTTATAGTG 127

Qy 1245 ATTAGGAAAGAGGTAGACATGTTACTTCAATCGATCAGAGACTTCTATGGAAGA 1304

Db 126 ATTAGGAAAGAGGTAGACATGTTACTTCAATCGATCAGAGACTTCTATGGAAGA 67

Qy 1305 TGACGATGTTGGAACAAAGTTCATCTCCACACTACTGTATATGGCATGCTCGAGCTCG 1364

Db 66 TGACGATGTTGGAACAAAGTTCATCTCCACACTACTGTATATGGCATGCTCTTGAGAG 7

Qy 1365 C 1365

Db 6 C 6

RESULT 8

AY104802

LOCUS Zea mays PC069597 mRNA linear HTC 18-FEB-2005

DEFINITION Zea mays PC069597 mRNA sequence.

ACCESSION AY104802

VERSION AY104802.1 GI:21207880

KEYWORDS HTC.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1429)

AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, P., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H. Jr.

TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization

JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)

REFERENCE 2 (bases 1 to 1429)

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 3 (bases 1 to 1429)

AUTHORS Coe, E.H.

TITLE Direct Submission

JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Location/Qualifiers

1..1429

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="MaizeGDB:633782"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public

contigs to seed Dupont contigs; this resource assembled by DuPont as part of a collaborative overgo addressing of BACs in conjunction with Mapping Project"

ORIGIN

Query Match 42.2%; Score 576.2; DB 4; Length 14
Best Local Similarity 75.7%; Pred. No. 5.2e-159;
Matches 727; Conservative 0; Mismatches 233; Indels 1;

Qy 35 GGTTCGTCAGAGGGGAGGCGAGAGGTGGGCAATGCGGTCATATGCG 94

Db 210 GGTTCGTCAGAGGGGAGGCGAGAGGTGGGCAATGCGGTCATATGCG 269

Qy 95 CGGCAGATAGAGCAGCTCTCGGAGTGCAGCGCTTGTGCGGAGTTCGAGGT 154

Db 270 CGGCAGATCTCGAGCTCGGGATTGCAAGTTCTCTGCTGAGGCGGAGGT 329

Qy 155 TGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGGAACTGCGAGCCCC 213

Db 330 TGGCAGCAGGCCAAGCGGATCTCATGAGGAGTGGAACTGCGAGCCCC 389

Qy 214 TGTACGGTTTCGGTGCATCCATGGCCAGTTTCATGATCTCATCGAGC 273

Db 390 CGTCACTGTCTGCGGCGACATCCACGGCCAGTTCTACGACCTCATCGAGC 449

Qy 274 AGGAGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGGACTATGCG 333

Db 450 CGGTGGCGACCGCCCGACACCACTACTCTTTATGGCGGACTACGTCC 509

Qy 334 TTATTCTGTGAGACTGTGTCGCTCTTAGTGGCCCTGAAAGGTGCGGTATA 393

Db 510 CTACTCAGTCAGACTGTGTCTTATTGGTGGCTCTAAAGTACGTTATF 569

Qy 394 CACATCTTTCGAGGGAACACGAGAGCAGCAGATTCAGCAAGTATATC 453

Db 570 CACAATATTGAGAGGAATCATGAGAGTAGACAAATAACTCAAGTGTATC 629

Qy 454 TGAATGCTCGGAGTATGAAATGCGAATGTTTGGAAAGTACTTTCACGC 513

Db 630 TGAATGCTCGGAAATATGAAATGCGAATGTTTGGAAAGTACTTTCACGC 689

Qy 514 CTACCTGCTCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTCTTCATC 573

Db 690 TTATTGCTCTCACAGCTCTTAGAATAATCAGATCTTCTGCTACATC 749

Qy 574 TCCATGCTGCACACATTCATGATCATCCGAGCCCTAGATCGTATTCACG 633

Db 750 TCCATGCTGCACACATTCATGATCATCCGAGCCCTAGATCGTATTCACG 809

Qy 634 CGAGGCGCGATGTGATCTACTCTGCTGATCCAGATGATCGTTGTC 693

Db 810 TGAAGGACCTATGTGATCTTTTGTGCTGACCCGGATGACAGATGTC 869

Qy 694 TTCACCGAGGTGCGGTTATCTTTTGGTCAAGATATTCAGAGCAGT 753

Db 870 TTCACCGAGGTGCTGATACATTTGGCGCAGATATTCACACAAAT 929

Qy 754 CAATGGTCTAAGTTTGGTTCACCGTGTCCACAGCTTGTGATGGAAGGAT 813

Db 930 AAATGGGCTAAGTCTTATTTCAAGAGCTCATCAACTTGTAAATGGAAGGGT 989

Qy 814 CCAGGATAAATGTTGTACAGTTTTCAGTGGCCCAATTTACTGTTAC 873

Db 990 CCAGGATAAAGCTGTGACAGTGTTCAGCGCCCTAACTATTGCTAC 1049

Qy 874 CATGCGCCCATATAATGGAGATAGATAAACAATGAATCGGCTTTTCTTC 933

Db 1050 CATGCTGGATCTCGAAATTTGGCGAACAATGATCAGAACTTCTTCC 1109

Qy 934 AGCACCGCGCAAGTGAACAGATGTGACCGGAAAGACTCCTGATTAAT 993

Db 1110 AGCTCCGCGGAGATTGAGCGGACATGACGCGCAAGACCCAGACTACT 1169

he
ize

Schachter V., Weissenbach J., Salanoubat M.
URGV INRA, Clermont-C. Cabocle M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
[http://www.genoscope.cns.fr/externes/sequences/Banque_Projet_EF/Full
length](http://www.genoscope.cns.fr/externes/sequences/Banque_Projet_EF/Full_length)
<http://www.genoscope.cns.fr/cgi-bin/qzb/qzb?source=Arabidopsis>.

FEATURES	source	Location/Qualifiers
		1. .1283
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		/mol_type="mRNA"
		/db_xref="taxon:3702"
		/clone="GSLFPB492D06"
		/tissue_type="Flowers and buds"
		/ecotype="Col-0"
gene		/plasmid="pCMVSPORT 6"
		complement(1. .1283)
ORIGIN		/gene="At1g10430"
Query Match	42.1%;	Score 574.2; DB 4; Length 1283;
Best Local Similarity	76.0%;	Pred. No. 2e-158;
Matches	708; Conservative	0; Mismatches 223; Indels 0; Gaps 0;
Qy	61	GGTTGGACAAATGCCGTCATATGACAGATGTAGACCGGCAGATAGAGCAGCTGTCCGAGTG 120
Db	166	GCTTTTTCAAGATGCCGTGCGAACGAGAGATCGACCGTCAGATCGACAGCTGTGAGAGTG 225
Qy	121	CAAGCCGTTCTCGAGTTGGAGGTGGAAGAACCTATGTGATCAAGCTCGGACGATCTTGTT 180
Db	226	TAAACCGTTATCGAGGCGGATGTGAGAGCGCTTTTGGCATCAAGCGAGAGCGATCCTTGT 285
Qy	181	GGAGGAGTGAACCGTGCAGCCCGTGAAGTGTCTGTGCACGCTTTTGGCGTGACATCCATGG 240
Db	286	CGAGGAATAAATGTTTCAGCCGGTGAAGTGTCTGTATCCGTTTGGCGCGATTTTCACGG 345
Qy	241	CCAGTTTTCATGATCTCATCGAGCTTTTCCGATAGGAGCGAAGCGCCCGACACGAACTA 300
Db	346	CCAGTTTATAGACCTTATTGAGCTCTTTTCGTATCGGTGGCAACGCTCTGTACTAACTA 405
Qy	301	CTTGTTCATGGCGGCACTATGTGGATCTGTGATATATTCTGTGAGACTGTGTGCTCTTT 360
Db	406	CCTCTTCATCGGAGACTATGTAGATCGTGGCTACTATTTCAGTAGAGACAGTTTCTCTATT 465
Qy	361	AGTGGCCCTGAAGTGGCGTATAGGATAGGATCACAATCTTGGCGGGGAACCAACGAGAG 420
Db	466	GGTGGCACTAAAGTGGCATACAGGGATAGACTTACAATCTTACGAGGGAATCACGAGAG 525
Qy	421	CAGGCAGATTACCGAAGTATATGTTTCTTATGATGAATGCTCGCGGAAGTATGGAATGC 480
Db	526	TCGGCAGATTACTCAAGTCTATGTTTTTATGACGAATGCTTGAGGAAGTACGGAATGC 585
Qy	481	GAATGTTTGGAAATPACTTACGGATCTGTTGCACTACCTGCGCTCTGAAGCTCTCATGTA 540
Db	586	TAAAGCTGTGGAAGTATTTTACAGACCTTTTTCGATTATCTTCTTACCGCCCTCATAGA 645
Qy	541	GCACGAGATTTTTTGCTCTTCATGTGTGCTGTCTCCATCGCTGCACATTTAGATTCAT 600
Db	646	GAGTCAGGTTTTCTGTTTGAATGAGGGCTTTTCACTTCTCTGGATACTCTTTGATAATAT 705
Qy	601	CCGAGCCCTAGATCGTATTCAAGAAGTGCOCGACGAGGGGCCGATGTGTGATCTTACTCTG 660
Db	706	CCGNAGCTTGGATCGGATACAGGAGGTTCCACACGAAGGACCTATGTGTGNTTTATTATG 765
Qy	661	GTCTGATCCAGATGATCGTTGTGGATGGGGCAATTTCCACAGAGGTGCCGGTTATACTTTT 720
Db	766	GTCTGATCCTTGATGATCGATGCGATGGGAATATCTCCACGAGGTGCTGGTTATACATT 825
Qy	721	TGGTCAAGATATTTCGACAGCGAGTTCAATCATATCAATGGTCTAAGTTTGGTTGCACTGC 780
Db	826	TGGAAGGATATCGACGCTCAATTTAATCAAAATGCGACTAAGTCTCATATCAAGAGC 885

Qy	781	TCACCAAGCTTGTGATGGAAGGATACAAATTTGGTGCAGGATATAAAATGTTG	
Db	886	GCATCAACTTGTTCATGGAAGGTTTTAACTGGTGTCAAGGATAAAGAATGTGC	
Qy	841	CAGTGGCCCCCAATTTACTGTTTACCGCTGTGGGAACATGGCCGCCATAATGG	
Db	946	TAGTGACCAACAATATTGCTACCGGTGTGGAACATGGCTGCCATCTAC	
Qy	901	AACAATGAATCGGTCTTTTCTTCAGTTTCGAACCCAGCACCGCGGCAAAAGTC	
Db	1006	GAACATGGAGCAAAACTTCTCCAGTTTCGATCCAGCTCCTCCGACAAAGTTC	
Qy	961	GAGCGGAGACCTCTGATTACTTTCTGTAA 991	
Db	1066	TACTCGGAAGACCCCTGATTATTTTTGTGA 1096	

RESULT 11	
CNS0AD99	
LOCUS	CNS0AD99 1285 bp mRNA linear
DEFINITION	Arabidopsis thaliana Full-length cDNA Complete sequence
ACCESSION	GSLTPEGH45ZH10 of Hormone Treated Callus of strain cc
KEYWORDS	Arabidopsis thaliana (thale cress).
SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana
REFERENCE	1 (bases 1 to 1285)
AUTHORS	Castell, V., Aury, J.M., Jaillon, O., Wincker, P., Clef Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schaeffer, G., Caboche, M., Weissenbach, J., and Salanoubat, V., Aury J.M., Jaillon O., Wincker P., Menard M., Clef Menard M., Weissenbach J., Salanoubat M.
TITLE	A Combined Approach to Evaluate and Improve Arabidopsis Annotation
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1285)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (18-Nov-2003) Genoscope - Centre National BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation. Aury J.M., Jaillon O., Wincker P., Menard M., Clef Menard M., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the genome released by MIPS (Munich Information Center for Sequences). 5 prime and 3 prime are assembled with the help of the Genoscope database. The sequences are available at http://www.genoscope.cns.fr/externe/sequences/Banque_lengths
FEATURES	Location/Qualifiers
source	1. 1285
	/organism="Arabidopsis thaliana"
	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/clone="GSLTPEGH45ZH10"
	/tissue_type="Hormone Treated Callus"
	/ecotype="Col-0"
	/plasmid="pCMVSPORT 6"
	complement(1..1285)
	/gene="Atlg10430"
gene	
ORIGIN	

Query Match	41.8%	Score 571;	DB 4;	Length 1285
Best Local Similarity	75.8%	Pred. No. 1.8e-157;		

Matches	706;	Conservative	0;	Mismatches	225;	Indels	0;	Gaps	0;
Qy	61	GGTTGGACAATGCGCTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTGCGAGTG	120						
Db	166	GCITTTTCAAGATGCCGTGGAACCGAGATCTGGACCGTCAGATCGACGAGCTGATGGATG	225						
Qy	121	CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCATTATGTGATCAAGCTCGGACGATCTTGTT	180						
Db	226	TAAACCGTTATCGGAGCGGATGTGAAGACGCTTTTGGGATCAAGCGAGAGCGATCTCTTGT	285						
Qy	181	GGAGGAGTGGAAAGCTGCAGCCGTTGAAGTGTCTGTCAACGCTTTTGGCGTGACATCCATGG	240						
Db	286	CGAGGAATAATATGTTTCAGCCGTTGAAGTGTCTGTTCACCGTTTTCGGCGATATTCACGG	345						
Qy	241	CCAGTTTTCATCATCTCATTCGAGCTTTTCCGATAGGAGCGAAGCGCCCGACACGAACTA	300						
Db	346	CCAGTTTATGACCTTATTCGAGCTCTTTCGTATCGGTGGCAACGCTCTCATACTAACTA	405						
Qy	301	CTTGTTTCATGGCGGACTATGTGGATCTGGATATATTTCTGTGCGAGACTGTGTGCGTCTTT	360						
Db	406	CCTCTTTCATGGGAGACTATGTAGATCTGGCTACTATTTCAGTAGAGACAGTTTCTCTATT	465						
Qy	361	AGTGGCCCTCAAGTGCGGTATAGGATAGGATACACAACTCTCGAGGGGAACACCGAGAG	420						
Db	466	GGTGGCACTAAAGTGCATACAGGATAGACTTCAACTCTTACAGGGGAATCACGAGAG	525						
Qy	421	CAGCGAGATTACGCAAGTATATGGTTTCTATGATGAATGCTCGGGAAGTATGGAATGC	480						
Db	526	TCGCGAGATTACTCAAGTCTATGGTTTTTATGAGGAATGCTTGAGGAAGTACGGAAATGC	585						
Qy	481	GAATGTTTGAAGTACTTACGGNATCTGTTTCGACTACTCTGCTCTGACAGCTCTCATTTGA	540						
Db	586	TAAACGCTCGGAAGTATTTTACAGACCTTTTTCGATATCTTCTCTTACCGCCCTCATAGA	645						
Qy	541	GCACGAGATTTTGTCTTCAATGCTGTCTGTCTCCATCGCTCGACACATTAGATCACAT	600						
Db	646	GAGTCAGTTTTTCTGTTTGCATGAGGGCTTTTCACTTCTCTGGATACTCTTGATATAT	705						
Qy	601	CCGAGCCCTAGATCGTATTTCAAGAAGTGC CGCACGAGGGCCGATGTGTGATCTACTCTG	660						
Db	706	CCGAAGCTTGGATCGGATACAGGAGGTTCCACACGAAGGACCTATGTGTGATTTATTATG	765						
Qy	661	GTCTGATCCAGATGATCGTTGTGATGGGGCATTTTACAGAGGTCGCGGTTTATCTTTT	720						
Db	766	GTCTGATCTCGATGATGCGATGGGAAATATCTCCAGAGGTCTGGTTATACATT	825						
Qy	721	TGGTCAAGATATTGCAGACGAGTTTCAATCATACCAATGGTCTAAGTTTGGTGCACGTGC	780						
Db	826	TGGNACGAGTATCGCAGCTCAATTTATCAACANATGGATAGTCTCATATCAAGAGC	885						
Qy	781	TCACCAGCTTGTGATGGAAGGATACAAATGGTGCAGGATAAAAAATGTTGTCAAGTTTTT	840						
Db	886	GCATCAACTTGTATGGAAGGTTTTAACTGGTGTGAGGATAAAGAAATCTGGTGACTGTGTT	945						
Qy	841	CAGTGGCCCAATTTACTTTTACCGCTGTGGGACATGGCCCATATATGAGATAGATGA	900						
Db	946	TAGTGCACCAAACTATTGTCTACCGGTGTGAAACATGGCTGCCAATCTAGAGATAGAGA	1005						
Qy	901	AACAATGAATCGGTCTTTTCTTCAAGTTTTCGAACACGACACCGCGGCAAAAGTGAACACAGATGT	960						
Db	1006	GAACATGGAGCAAACTTCTCCAGTTTCGATCCAGCTCTCTCGACAGTTTGAACCTGTATC	1065						
Qy	961	GACGCGGAAGACTCCTGATTACTTTCTGTAA	991						
Db	1066	TACTCGGAAGACCCCTGATTATCTTTTGTGA	1096						

RESULT 12

CNS0ADNP	CNS0ADNP	1278 bp	mRNA	linear	HTC 06-FEB-2004
LOCUS	Arabidopsis thaliana	Full-length cDNA	Complete sequence from clone		
DEFINITION	GSUPE16A06 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).				
.	.				

ACCESSION	BX813410
VERSION	BX813410.1 GI:42473857
KEYWORDS	HTC; GSLT cDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
AUTHORS	Castelli,V., Aury J.M., Jaillon O., Wincker P., Clep Menard,M., Cruaud,C., Qutier,F., Scarpelli,C., Scha Temple,G., Caboche,M., Weissenbach,J. and Salanoubat V.. Aury J.M., Jaillon O., Wincker P., Menard M., Cr Schachter V., Weissenbach J., Salanoubat M.
TITLE	UVG INRA : Clepet C., Caboche M.
JOURNAL	Annotation is based on the June 2003 version of the genome released by MIPS (Munich Information center f
REFERENCES	Sequences). 5 prime and 3 prime are assembled with p
JOURNAL	http://www.genoscope.cns.fr/externe/sequences/Banque
COMMENT	length
	http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=A
FEATURES	Location/Qualifiers
source	1..1278
	/organism="Arabidopsis thaliana"
	/mol_type="mRNA"
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	/clone="GSLTFB16ZA06"
	/tissue_type="Flowers and buds"
	/ecotype="Col-0"
gene	/plasmid="pCMVSPORT 6"
	complement(1..1278)
ORIGIN	/gene="Atig10430"
Query Match	41.4%; Score 564.6; DB 4; Length 12
Best Local Similarity	75.4%; Pred. No. 1.4e-155;
Matches	702; Conservative 0; Mismatches 229; Indels
Qy	61 GGTTGGACAATGCCGTTCATATGCAGATGTAGACC CGGCAGATAGCAGC
Db	167 GCITTTCAAGATGCCGTTCGAACGAGATCTGGACCGTCAGATCAGCAGC
Qy	121 CAAGCCGTTTCGAGTTTGAGGTGAAGAACCATTATGTGATCAAGCTCGGA
Db	227 TAAACCGTTTATCGAGCGCATGTGAGGACGCTTTGCGATCAAGCGAGAG
Qy	181 GGAGGAGTGAAAGTGCAGCCGTCGAGTGTCTGTCTCACGTTTTTCGGGTG
Db	287 CGAGGAATAATATGTTTCAGCCGGTGAAGTGTCTGTATCCGTTTTCGGCGG
Qy	241 CCAGTTTTCATGATCTCATCGAGCTTTTCCGCATAGAGGCAAGCGCCCCG
Db	347 CCAGTTTTCATGATCTCATCGAGCTTTTCCGCATAGAGGCAAGCGCTCTG
Qy	301 CTGTTTCATCGGGCGACTATGTGGATCGTGATTAATTCTGTGAGACTGT
Db	407 CCTCTTCATCGGGCGACTATGTAGATCGTGGCTACTATTTCAGTAGAGACAG
Ov	361 AGTGGCCCTCGAAGTGGCGGTATATAGGATAGGATACCAATCTTTCGAGGGA

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467 GGTGGCACTAAAAGTGGCGATACAGGATAGACTTAACTCTTACAGGAATCACGAGAG 526
421 CAGGCGAGATTACCGAAGTATATGTTCTATGATGAATGCCCTCGGGAAGTATGGAATGC 480
527 TCGGCGAGATTACTCAAGTCTATGTTGTTTATACGAATGCTTGGGAAGTACGGAATGC 586
481 GAATGTTTGGAGTACTTACCGAGTCTGTTCCAGTACTGCTTCCAGTCTTCAATGGA 540
587 TAACGCTGGAAGTATTTACAGACCTTTTCGATTATCTTCTCTTACCGCCTCATAGA 646
541 GCACAGAGATTTTGTCTTATGTTGTTGTTCTGTTCTGATCGCTCGACATTAGATACAT 600
647 GAGTCAGGTTTCTGTTTGCATGAGGAGGCTTTTCACTTCTCTGGATATCTCTTGATAAT 706
601 CCGAGCCCTAGATCGTATTAAGAGTGCAGCAGGAGGCGGATGCTGATCTACTCTG 660
707 CCGAAGCTTGGATCGGATACAGGAGGTTCCACAGGAGGACCTATGTGTGATTTATTATG 766
661 GTCTGATCCAGATGATCGTTGTGGATGGGCAATTTCCACAGGAGTGGCGTTTACTTT 720
767 GTCTGATCTGATGATCGATGTTGGATGGGATATCTCCAGGAGTGTGTTTACTATT 826
721 TGCTCAAGATATTGAGAGGATCTCAATCATACCAATGCTTAACTTTGTTGTCAGCTGC 780
827 TGGACAGGATATCGCAGCTCAATTTAATAACAACAACTGAGCTTAACTCTCATATCAAGAGC 886
781 TCACAGCTTGTGGAAGGATACAAATTTGTCAGGATGAATGTTGTCACAGTTT 840
887 GCATCACTTGTGATGGAAGGTTTAACTGGTGTGAGGATGAATGTTGTTACTGTGT 946
841 CAGTGGCCCAATTAATCTGTTCCGCTGTTGGGAACATGTCGCGCATATATGAGATAGATGA 900
947 TAGTGACCAACATATTCTACCGGTGTGGAACATTTCTGCTCATTTAGAGATAGGAGA 1006
901 AACAAATGAATCGTCTTTTCTTCTAGTTGGAACAGCACCGGCGGCAAGAACAGATGT 960
1007 GTACATGAGCAAAATTTCTCCAGTTCGATCGATCGCTCTCGACAAATTTGAACCTGATAC 1066
961 GACGCGGAAGACTCTGATTAATCTTCTGTAA 991
1067 TACTCGGAAGACCCCTGATGTTGTTCTGTGA 1097

RESULT 13
AY108657
LOCUS AY108657 1534 bp mRNA linear HTC 25-FEB-2005
DEFINITION Zea mays PC069598 mRNA sequence.
ACCESSION AY108657
VERSION AY108657.1 GI:21211829
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 1534)
AUTHORS Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,
Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F.,
Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
Jr.
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 1534)
AUTHORS Haney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 1534)

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AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, Unive
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physi
these are publicly available from ZmDB and may be fc
searching at MSL, maizemap.org; ZmDB, www.zmdb.iast
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When th
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Schnable, Iowa State, then clones may be requested f
www.zmdb.iastate.edu.
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overgo addressing of BACs in conjunction wi
Mapping Project"
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REFERENCE 1 (bases 1 to 1250)
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
          Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
          Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
          A Combined Approach to Evaluate and Improve Arabidopsis Genome
          Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1250)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
          Life technologies (a division of invitrogen) members carried out
          full-length libraries construction : Temple G.
          Genoscope members carried out sequencing and annotation : Castelli
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          Schachter V., Weissenbach J., Salanoubat M.
          URGV INRA : Clepet C., Caboche M.
          Annotation is based on the June 2003 version of the Arabidopsis
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          Sequences) . 5 prime and 3 prime are assembled with Phrap.
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REFERENCE 1 (bases 1 to 849)
AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
          Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
          Wing,R.A.
          Global assembly of Cotton ESTs
          Unpublished (2004)
          Contact: Rod A. Wing
          Arizona Genomics Institute
          The University of Arizona
          Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: rwing@genome.arizona.edu
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Db 241 CGATTACGTAGATCGAGATATTACTCTGTGGAGACTGTCACTCTTTTAGTGGACTGAA 300
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 06:21:46 ; Search time 280 Seconds
(without alignments)
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Title: US-10-764-259-8

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Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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SUMMARIES

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6	505.2	37.0	2181	3	US-09-780-049-17
7	505.2	37.0	2182	3	US-09-949-016-5543
8	505.2	37.0	2966	3	US-09-780-049-3
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ALIGNMENTS

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; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
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; TYPE: DNA
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QY 841 CAGTGGCCCAATTAATCTGTTACCGTGTGGGAACATGCGCCCAATAATGGAGATAGTA 900
Db |||||
QY 901 AACATGAATCGCTCTTTCTTCAGTTTCAACAGCAGCAGCGCGCAAGTGAACAGATGT 960
Db |||||
QY 901 AACATGAATCGCTCTTTCTTCAGTTTCAACAGCAGCAGCGCGCAAGTGAACAGATGT 960
Db |||||
QY 961 GACGGGAAGACTCCTGATTAATCTTCTGTAACATGGCCCTATACATGGTACCTTTTACTT 1020
Db |||||
QY 961 GACGGGAAGACTCCTGATTAATCTTCTGTAACATGGCCCTATACATGGTACCTTTTACTT 1020
Db |||||
QY 1021 ACTGAATTGTTCTGTATAGTCACTTCCATGGAAGCAGTTTCCCTGAAATGAATACT 1080
Db |||||
QY 1021 ACTGAATTGTTCTGTATAGTCACTTCCATGGAAGCAGTTTCCCTGAAATGAATACT 1080
Db |||||
QY 1081 CCCTCATGATCTAGTATGATGAAGTATCTTCTTTGAAGTGTTCCTCCCTTTTACTA 1140
Db |||||
QY 1081 CCCTCATGATCTAGTATGATGAAGTATCTTCTTTGAAGTGTTCCTCCCTTTTACTA 1140
Db |||||
QY 1141 CTTGCTCTCTGTTCAATTCATAAAGTTGCTTCAGAAACAACTGAGATGTTGTGAATGTAA 1200
Db |||||
QY 1141 CTTGCTCTCTGTTCAATTCATAAAGTTGCTTCAGAAACAACTGAGATGTTGTGAATGTAA 1200
Db |||||
QY 1201 CTTGGAACAAGAGAGCAGTGTCAATGGTTGCAAGGTTATAGTATTAGGGAAGAAGGT 1260
Db |||||
QY 1201 CTTGGAACAAGAGAGCAGTGTCAATGGTTGCAAGGTTATAGTATTAGGGAAGAAGGT 1260
Db |||||
QY 1261 AGCAGATGTTACTCAAAATCGATCAGAGACTTCTATGGAAGATCAGATCGTGGAAAC 1320
Db |||||
QY 1261 AGCAGATGTTACTCAAAATCGATCAGAGACTTCTATGGAAGATCAGATCGTGGAAAC 1320
Db |||||
QY 1321 AACGTTTCATCTCCACACCTACTGTATATGGCATGTCTCGAGCTCGC 1365
Db |||||
QY 1321 AACGTTTCATCTCCACACCTACTGTATATGGCATGTCTCGAGCTCGC 1365
Db |||||

RESULT 2
US-09-780-045-3
; Sequence 3, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATA:
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 3
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (991)... (1920)
US-09-780-045-3

Query Match 37, 8%; Score 515.6; DB 3; Length 25
Best Local Similarity 69.7%; Pred. No. 1.2e-160;
Matches 698; Conservative 0; Mismatches 304; Indels

QY 14 GAGGAGAGAGCGGATCGGTTAGGGTTTGGTGGCCAGGGGGAGGCGAGAGGT 73
Db ||||| 1002
QY 943 GCGGCGCGCGGCTGGGCTCGGGATCCGATCGGATCGGCGCGCAT 133
Db ||||| 1062
QY 74 CCGTCATATGAGATGTAGACCGGAGATAGAGAGAGCTGTGCGAGTGCA 193
Db ||||| 1122
QY 1063 GAGAACCAAGTGCAGACGCTGTGCGAGAAAGCAAGGAAATTTTAAACAA 253
Db ||||| 1182
QY 194 GTGAGCCCGTGAAGTGTCTGTCAACGTTTGGGTGACATCCATGGCCA 313
Db ||||| 1242
QY 1123 GTGAGAGGTTGTTGCCCTGTACTGTCTGTGAGATGTGATGGTCA 373
Db ||||| 1302
QY 254 CTATTCGAGCTTTTCCGATAGAGAGCAAGCGCCGACACGAACTACTT 433
Db ||||| 1362
QY 1183 CTTATGGAACTCTTTAGAAATGGTGGAAATCAACCGGATACAACTACTT 493
QY 314 GACTATGTGGATCGTGGATATATTCTGTGAGACTGTGCTCTTACTT 1422
Db ||||| 553
QY 1243 GACTATGTAGACAGAGGATATATTCTAGTGGAGACTGTGACTCTTCTTGT 1482
Db ||||| 613
QY 374 GTGCGGTATAGGGATAGGATCACAACTCTGCGAGGGAACACGAGAGCAG 1542
Db ||||| 673
QY 1303 GTGCGTTATCCAGAACGCAATTAACAATTTGAGAGGAATCACGAAAGCG 1602
QY 434 CAAGTATATGTTTCTATGATGAATGCTGCGGAAGTATGGAATTCGAA 733
Db |||||
QY 1363 CAAGTATATGGCTTTTATGATGAATGTCTGCGAAAGTATGGGAATGCCAA 733
QY 494 TACTTTCAGGATCTGTTCCGACTTACTGCTCTGACAGCTCTCATTTAGCA 733
Db |||||
QY 1423 TATTTTACAGATCTCTTTGATTAATCTTCCACTTACAGCTTTAGTAGATGG 733
Db |||||
QY 554 TGTCTTCAATGGTGTCTGTCTCCATCGCTCGACACATTTAGATCAATCCG 733
Db |||||
QY 1483 TGCCTCCATGTGGCTCTCTCCATCCATAGACACACTGGATCATATAAG 733
Db |||||
QY 614 CGTATTCAGAAAGTGCAGCAGAGGCGCGATGTGTACTACTCTGCTC 733
Db |||||
QY 1543 CGTTTACAGGAAGTTCCACATGAGGGCCCAATGTGTGATCTGTTATGGTC 733
QY 674 GATCGTTGTGATGGGCAATTTCCACAGAGGTGCGGTTTACTTTTGG 733
Db |||||

Qy	86	GATGTAGACCGGAGATAGACAGACTGTGCGAGTGCAGACCGCTTGTGTCGAGATTGGAGGTG	145
Db	46	GAGCTGGACAGCTGGGTCCAGCAGCTGAACAGAGTGTAAAGCAGCTGAACAGAGAACCAAGTGT	105
Qy	146	AAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGGATGGAACGTGCGACCCCGTG	205
Db	106	CGGACGCTGTGCGAGAGCGCAAGGAAATTTTAAACAAAGAATCAAAATGTGCGAAGAGGTT	165
Qy	206	AAGTGTCTGTCAACGGTTTGGCGTGACATCCATGGCCAGCTTTTCATGATCTCATCGAGCTT	265
Db	166	CGTTGGCCCTGTTACTGTCTGTGGAGATGTGATGGTCAAATTCATGATCTTATGGAACTC	225
Qy	266	TTCCGCAATAGGAGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGCATATGTGGAT	325
Db	226	TTTAGAAATTTGGTGGAAAAATCAACGGATACAAACTACTTAATTCATGGGTGACTATGTAGAC	285
Qy	326	CGTGGATATATTCTGTGAGACTGTGTGGCTCTTACTGTGGCCCTGGAAGTGGCGGTATAGG	385
Db	286	AGAGGATATATTTCAGTGGAGACTGTGACTCTTCTTGTGACNTTAAAGTGGCGTATATCCA	345
Qy	386	GATAGGATCACAATCTTGCGAGGGAACACAGAGACGAGCAGATTACCGAAGTATATGGT	445
Db	346	GAACGCAATTACAAATTTAGAGAGAAATCAACGAAAGCCGACAAATTACCCAAGTATATGGC	405
Qy	446	TTCTATGATGAATGCTTCGGAAGTATGGAAATGCGAATGTTTGGAAAGTACTTCACGGAT	505
Db	406	TTTTTATGATCAATGTCTCGAAAGTATGGGAATGCCAACGTTTGGAAATATTTTACAGAT	465
Qy	506	CTGTGTCGACTACTCGCTCTGACACTCTCAATTGAGCACGAGATTTTTTCTCTTCATGGT	565
Db	466	CTCTTTGATATCTTCCACTTACAGCTTTAGTAGATGGACAGATTAITCTGCCTCCATGGT	525
Qy	566	GGTCTGCTCCATCGCTCGACACATTAGATCACATCCGAGCCCTAGATCGTATTTCGAAGAA	625
Db	526	GGCCTCTCTCCATCCATAGACACACTGGATCATATAGAGCCCTGGATCGTTTACAGGAA	585
Qy	626	GTCCGCGACGAGGGCCGATGTGTGATCTACTTGGTCTGATCCAGATGATCGTTGTGGA	685
Db	586	GTTCACATAGAGGGCCAAATGTGTGATCTGTATTGGTCCAGATCCAGATGATCGTGGTGA	645
Qy	686	TGGGGCAATTTCAACGAGGTCCCGGTTACTTTTGGTCAAGATATGACAGAGCAGTTC	745
Db	646	TGGGGTATTTTCAACCACTGGTCTGGCTGACATTTTGGACAAGACATTTCTCGAAACCTTT	705
Qy	746	AATCATACCAATGGTCTAAGTTTGGTGTGACGCTGCTCACCGCTTGTGTGATGGAGGATAC	805
Db	706	AACCATGCCAATGGTCTCACCTGGTTCTCGTGCCACACAGCTTGTAAATGGAGGATAC	765
Qy	806	AATTGGTGCCAGGATAAAATGTTGTCAAGTTTTCAGTGTCCCCCAATTACTGTACCGC	865
Db	766	AATTGGTGTCAATGATCGGAAATGTGGTTACCAATTTTCAGTGCACCCAATTACTGTATCGT	825
Qy	866	TGTGGGAAATGTCGCCCAATATGAGATAGATGAAACAAATGAATCGGTCTTTTCTTCAG	925
Db	826	TGTGGGAAACAGGCTGCTATCATGGAATTAGATGACACTTTTAAATATATCTCTTCCTCAA	885
Qy	926	TTCCGAACACGACCGCGGCAAAAGTGAAACAGATGTGACGCGGAAGACTCTCTGATTACTTT	985
Db	886	TTTGACCGCGGCTCGTGTGTGAGCTCATGTTACGCGGCGCAACCCAGACTACTTTC	945
Qy	986	CTGTAACATGGCCTATATCATGGTACCTTTT	1015
Db	946	CTATAAATTTCTCTGGGAAACCTGCCTTTT	975

RESULT 5

RES001 3
US-09-780-045-10
; Sequence 10, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B

926 TTGAAACGACGACCGCGGCAAGTGAACAGATGTGACGCGGAAGACTCTGTGATTACTTT 985
 1174 TTTGACCCAGCACTCGTCTGGAGAGCCTCATGTGACCGGGCGCACCCAGAGACTATTC 1233
 986 CTGTAAA 992
 1234 CTATAAA 1240

RESULT 6

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US-09-780-049-17
; Sequence 17, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; FILE REFERENCE: RTS-0114
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 17
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1139)
US-09-780-049-17

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Query Match	37.0%	Score 505.2;	DB 3;	Length 2181;
Best Local Similarity	69.1%;	Pred. No. 3.2e-157;		
Matches 690;	Conservative	0;	Mismatches 308;	Indels 0;
			Gaps 0;	

10	QC	CGCGAGGAGACGGATCGGTTAGGGTTGGTCCACGGGGGAGGGCAGAGTTGGAC	69		
158	DB	GC	CGCGCGCGGAGGAGCGCGAGCGCGACCGGCTGGGCGGGTGGCATCATGACAG	217	
70	QY	AATGCCGTATATGCAGATGTAGACCGGAGATAGAGCAGCTGTCGGAGTGC	129		
218	DB	GAAGGTGTTCCAAAGAGCTGCACCATGTCGATCGAGCAGCTGAA	277		
130	QY	GTCGGAGTTGGAGGTGAAGAACCCTATGTGATCAAGCTCGACAGCTCTTG	189		
278	DB	GTC	CGAGTCCCAGTCAAGAGCCTCTGCGAGAGGCTTAAGAAATCCTGACAAAGATC	337	
190	QY	GAACGTGCAGCCCGTGAAGTGTCTGTGACGGTTTGGGTGACATCATGGCCAGTTTCA	249		
338	DB	CAACGTGCAAGAGGTTTCGATGTCCAGTTACTGTCTGTGGAGATGTGATGGGCAATTTCA	397		
250	QY	TGATCTCATCGAGCTTTCCGCATAGGAGCAAGGCCGCCGACACGAACTACTTGTTCAT	309		
398	DB	TGATCTCATGGAACCTGTTAGAAATGGTGCAATCAACAGATACAAATTACTTGT	457		
310	QY	GGCGGACTATGTGGATCGTGGAATATTCTGTGAGACTGTGTGCTCTTAGTGGCCCT	369		
458	DB	GGGAGATTATGTTGACAGAGGATATTATTGAGTTGAAACAGTTACACTGCTGTGAGCTCT	517		
370	QY	GAAGTGC	CGGTATAGGATAGATCAAAATCTTTGCGAGGGAACCAAGAGCAGGAGAT	429	
518	DB	TAAGGTT	CGTTACCGTGAA	CGCATCAACATCTTCGAGGGAATCATGAGAGCAGACAGAT	577
430	QY	TACGCAAGTATATGGTTTCTATCATGAATGCCCTGCGGAGATATG	489		
578	DB	CACACAAGTTTATGGTTTCTATGATGAAATGTTTAAAGAAATATG	637		
490	QY	GAAGTACTTTCACGGATCTGTTCCAGTACCTGCCTCTGACAGCTCTCATTTAGC	549		
638	DB	GAATAATTTTACAGATCTTTTTCAGCTATCTTCTCTACCTGCCTTGGTGATGGG	697		
550	QY	TTTTTGTCTTTACGTGGGTCTGTCTCCATCGCTCGCACATTTAGATCA	609		

[illegible]

RESULT 7

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US-09-949-016-5543
; Sequence 5543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5543
; LENGTH: 2182
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5543

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Query Match	37.0%	Score 505.2	DB 3	Length 21
Best Local Similarity	69.1%	Pred. No. 3.2e-157		
Matches 690	Conservative	0	Mismatches 308	Indels
Qy	10	GC	CGGAGGAGCGGATCGGTTAGGGTTTGGTCCAGGGGGGAGGGCAG	AC 69
Db	159	GC	GGCGCGCGGAGAGCGCGGAGCGGACGCCGCTGGGGCGGGTGGCA	3A 218
Qy	70	AATGCCGTCATATG	CAGATGTAGACCGGCAGATAGAGCAGCTGTCTCGAGT	TT 129
Db	219	GAAGGTGTTCAACA	AGGAGCTGGACCAAGTCGAGCAGCTGAACAGT	CT 278
Qy	130	GTCCGAGTTGGAGGTGAAGAA	CCTATGTGATCAAGCTCCGACGATCTTGC	TG 189
Db	279	GTCCGAGTCCCGAGTCAAGAGC	CTCTGCGAGAGGCTAAAGAAATCCTGA	TC 338

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QY 190 GAACTGTCAGCCCGTGAAGTGTCTCTGTCACCGTTTGGCGTGACATCCATGCCAGTTTCA 249
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 339 CAACGTGCAAGAGGTTCGATGTCAGTGTACTGTCTGTGGAGATGTGCATGGCAATTTCA 398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 TGATCTCATCAGACTTTTCCGCATAGGAGGCAAGCGCCCGACACGAACTACTTGTTCAT 309
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 399 TGATCTCATGGAAGTGTAGAAATGGTGGCAAAATCACCAGATACAAATTAATTGTTAT 458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 310 GGGCGACTATGTGGATCGTGGATATATATCTGTGTGAGACTGTGTGCGTCTTAGTGGCCCT 369
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 459 GGGAGATTATGTGACAGAGGATATTAATTCAGTTGAAACAGTTACACTGCTTGTAGCTCT 518
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 370 GAAGTGGCGGTATAGGATAGATACAAATCTTTCGAGGGAACACGAGACAGCAGAT 429
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 519 TAAGTGTCTTACCGTGAACGATCACCATTCTTCGAGGGAATCATGAGAGGACAGAT 578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 430 TACGCAAGTATATGTTTCTATGATGAATGCCGCGGAAGTATGGAATGCGAATGTTTG 489
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 579 CACACAAGTTATGTTTCTATGATGAATGTTAAGAAATATGGAATGCAATGTTG 638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 GAACTACTTCAGGATCTGTGCACTACCTGCTCTGACAGCTCTCATTTGAGCAGAGAT 549
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 639 GAAATATTTTACAGATCTTTTTCAGTATCTCTCTCACTGCTTGTGTGATGGCAGAT 698
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 550 TTTTGTCTTCATGCTGTGTCTCTCCATCGCTCGACACATTAGATCACATCCGAGCCCT 609
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 699 CTTCGTCTACATGTTGTCTCTGCCATCTATAGATACACTGGATCATATCAGAGCACT 758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 610 AGATCGTATTCAAGAAGTCCCGCAGCGAGGCGCGGATGTGTGATCTCTGCTGTATCC 669
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QY 759 TGATCGCTTACAAGAAGTTCCCATGAGGGTCCAAATGTGTGACTTGTGTGATCC 818
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 670 AGATGATCGTTGTGATGGGCAATTTACCAGAGGTGCGGTTATATCTTTTGTGTCAGA 729
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QY 819 AGATGACCGTGTGTGGGTATATCTCTCGAGGAGCTGGTTACACCTTTGGGCAAGA 878
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 730 TATTGACAGCAGTTCAATACATACCAATGGTCTAGTTTGGTTGACGTCTACCACT 789
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QY 879 TATTCTCAGACATTAATCATGCAATGGCTCAGTTGGTGTCTAGAGCTCACCACT 938
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QY 790 TGTGATGGAAGGATACAAATTTGTGCGAGGATAAAATTTGTTCAGTGTTCAGTGCCCC 849
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 939 AGTGATGAGGATATACTGTGCTCATGACCGGAATGTAGTAAAGATTTTCAGTGCTCC 998
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 850 CAATTAATCTTACCCTGTGGGAAATGCGCCCATATATGAGATAGATGAACAAATGAA 909
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 999 AAATTAATTTATCGTTTGTGTTAAACCAAGCTGCAATCATGGAATTTGACGATCTTAA 1058
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 910 TCGGTCTTTTCTCAGTTGCAACGACCGCGGCAAGTGAACAGATGTGACGCGGA 969
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1059 ATACTCTTTTCTTTCAGTTTTCACCGACCTCTGTAGAGCGGACCATGTTACTCGTCG 1118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 970 GACTCTCTGATTCTTCTTAAACATGGCTTATACATG 1007
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1119 TACCCAGACACTTCTCTGATGAATTTTAAACTTG 1156
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 8
US-09-780-049-3
; Sequence 3, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780, 049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 3
; LENGTH: 2966
; TYPE: DNA

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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (995)...(1924)  
US-09-780-049-3  
  
Query Match 37,08; Score 505.2; DB 3; Length 29;  
Best Local Similarity 69.18; Pred. No. 3.9e-157;  
Matches 690; Conservative 0; Mismatches 308; Indels  
3 0;  
  
QY 10 GCGCGGAGGAGCGGATCGGTTAGGGTTTGGTCCCGAGGGGAGGGCAG. C 69  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| aA 1002  
QY 943 GCGCGCGCGGAGGAGCGGAGCGCGCGCTGGGCGGGTGGCA T 129  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1062  
QY 70 AATCCGCTCATATCCAGATGTAGACCGGCGAGATAGAGCAGCTGTGGAGT X 189  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| G 1122  
QY 130 GTCGGAGTTGGAGGTGAAGACCTATGTGATCAAGCTCGGACGATCTTGG C 249  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| A 1182  
QY 190 GAACTGCGAGCCCGTGAAGTGTCTCTGTCACGGTTTGGCGTGACATCCATG T 309  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1242  
QY 310 GGGCGACTATGTGATCGTGGATATTTCTGTCGAGACTGTGTGCGTCT T 369  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1302  
QY 1243 GGGAGATATGTTGACAGAGGATATTTTCAAGTTGAACAGTTACACTGC T 429  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1362  
QY 370 GAAGTGGCGGTATAGGATAGGATCACAATCTTCGAGGGAACACCGAGA T 489  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1422  
QY 1303 TAAGTTCGTTTACCGTGAACGATCACCATTCTTCGAGGGAATCATGAGA T 549  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1482  
QY 430 TACGCAAGTATATGGTTTCTATGATGAATGCTCTCGGGAAGTATGGAAATG T 609  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1542  
QY 1363 CACACAAGTTTATGGTTTCTATGATGAATGTTTAAAGAAAATATGGAAATG T 669  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1602  
QY 490 GAACTACTTCAGGATCTGTTTCGACTACCTGCGCTCTGACAGCTCTCAATG T 729  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1662  
QY 1423 GAAATATTTTACAGATCTTTTGTACTATCTCTCACTGCTTGGTGG T 789  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1722  
QY 550 TTTTGTCTTCATGCTGTGTCTCTCCATCGCTCGACATTAGATCACA T 849  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1782  
QY 1483 CTTCTGCTCATGTTGGTCTCTCGCCATCTATAGATACACTGGATCATA T 909  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1842  
QY 610 AGATCGTATTCAAGAAGTCCCGACGAGGCGCGCATGTGTGATCTACTCT T 969  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1902  
QY 1543 TGATCGCCTACAGAAAGTTCCCCATGAGGGTCCAAATGTGTGACTTGTCT T 999  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1902  
QY 670 AGATGATCGTTGTGATGGGCAATTTCAACACAGAGTGC CGGTTATACCT T 789  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 789  
QY 1603 AGATGACCGTGGTGGGTATATCTCTCGAGGAGCTGTTACACCT T 1722  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 849  
QY 730 TATTGCAAGCAGTTTCAATACATACCAATGGTCTTAAGTTTGGTTGCACGCTG T 1782  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 849  
QY 1663 TATTCTGAGACATTTAATCATGCCAATGGCTCACGTTGGTGTCTAGAG T 1782  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 849  
QY 790 TGTGATGGAAGGATACAAATTTGGTGGCGAGGATAAAATGTTGTGTCAAGTTT T 1782  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 849  
QY 1723 AGTGATGAGGAGATATAACTGTGTGCCATGACCGGAAATGTAGTAACGATTT T 1782  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 849  
QY 850 CAATTAATCTTACCGCTGTGGAACATGCGCGCATATATGAGATAGATGAGATG T 909  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1842  
QY 1783 AAATTAATTTTATCGTTGTGTGTTAAACAGCTGCAATCATGGAACCTTGAG T 969  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1902  
QY 910 TCGGTCTTTTCTTCCAGTTTGAACACGACCGCGGCAAGTGAACAGATG T 969  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1902  
QY 1843 ATACTCTTTTCTTCCAGTTTGAACACGACCGCGGCAAGTGAACAGATG T 969  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| T 1902
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Oy	970	GACTCCTGATTAC	TTC	TGTAAACA	TGGCC	TATACATG	1007
D6	1903	TACCCAGACTCTT	CCTGTAA	TGAAA	TTTAAAA	CTTG	1940

```

RESULT 9
US-09-300-958A-39
; Sequence 39, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nu
; FILE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-39

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Query Match 36.7%; Score 501.2; DB 3; Length 1787;

Position	Reference	Sample	Match	Mismatch	Indel	Gap
86	GATGTAGACGGCAGATAGAGCAGCTCTCGAGGTGCAAGCGTGTTCGAGATTGAGAGTG	86	GATGTAGACGGCAGATAGAGCAGCTCTCGAGGTGCAAGCGTGTTCGAGATTGAGAGTG	145		
207	GAGCTGGACGAGTGGATCGAGCAGCTGAAAGAGTGCAGCAGCTGTCCGAGTCCAGGTC	207	GAGCTGGACGAGTGGATCGAGCAGCTGAAAGAGTGCAGCAGCTGTCCGAGTCCAGGTC	266		
146	AAGAACTTATGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGGAAACGTGCAGCCCGTG	146	AAGAACTTATGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGGAAACGTGCAGCCCGTG	205		
267	AAGAGCCTCTCGCAGAGGCTAAAGAAATCTGACAAAGAAATCCAAACGTCGAAAGGTT	267	AAGAGCCTCTCGCAGAGGCTAAAGAAATCTGACAAAGAAATCCAAACGTCGAAAGGTT	326		
206	AAGTGCTCTGACGTTTCGGGTGACATCCATGGCCGAGTTTCATGATCTCATCGAGCTT	206	AAGTGCTCTGACGTTTCGGGTGACATCCATGGCCGAGTTTCATGATCTCATCGAGCTT	265		
327	CGATGTCGAGTTACTGTCTGTGGAGATGTGATGGGCAATTTTCATGATCTCATGGAAC	327	CGATGTCGAGTTACTGTCTGTGGAGATGTGATGGGCAATTTTCATGATCTCATGGAAC	386		
266	TTCCGCATAGAGGCAAGCGCCCGACACGAACTTACTTGTTCATGGCGGACTATGTGAT	266	TTCCGCATAGAGGCAAGCGCCCGACACGAACTTACTTGTTCATGGCGGACTATGTGAT	325		
387	TTTAGAATTGGTGGCAATCACCAGATACAAATTACTTGTATTGGAGATTAATTGTGAC	387	TTTAGAATTGGTGGCAATCACCAGATACAAATTACTTGTATTGGAGATTAATTGTGAC	446		
326	CGTGGATATTATTCTGTTCGAGACTGTGTCTCTTACTGGCCCTGGAAGTGCGGTATAGG	326	CGTGGATATTATTCTGTTCGAGACTGTGTCTCTTACTGGCCCTGGAAGTGCGGTATAGG	385		
447	AGAGGATATTATTTCAGTTGAAACAGTTTACACTGCTTGTAGCTCTTAAGTTTCGTTACCGT	447	AGAGGATATTATTTCAGTTGAAACAGTTTACACTGCTTGTAGCTCTTAAGTTTCGTTACCGT	506		
386	GATAGGATCAATCTTCGAGGGAACACGAGAGCAGGACAGATTACGCAAGTATATGGT	386	GATAGGATCAATCTTCGAGGGAACACGAGAGCAGGACAGATTACGCAAGTATATGGT	445		
507	GAACGCATCACCATCTTTCGAGGGAATCATGAGAGCAGACAGATCACACAAGTTTATGGT	507	GAACGCATCACCATCTTTCGAGGGAATCATGAGAGCAGACAGATCACACAAGTTTATGGT	566		
446	TTCTATGATCAATGCTTCGGAAGTATGGAATATGCGAATGTTTGGAGTAGTACTTCACCGAT	446	TTCTATGATCAATGCTTCGGAAGTATGGAATATGCGAATGTTTGGAGTAGTACTTCACCGAT	505		
567	TTCTATGATCAATGTTTAAAGAAATATGGAATATGGAATGTTTGGAAATATTTTACAGAT	567	TTCTATGATCAATGTTTAAAGAAATATGGAATATGGAATGTTTGGAAATATTTTACAGAT	626		
506	CTGTTTCGACTACCTGCTCTGACAGCTCTCATTTGAGCACGAGATTTTTTGTCTTTCATGGT	506	CTGTTTCGACTACCTGCTCTGACAGCTCTCATTTGAGCACGAGATTTTTTGTCTTTCATGGT	565		
627	CTTTTTGACTATCTTCTCTCTCACTGCTTGGTGGATGGGCAGATCTTCTGTCTACATGGT	627	CTTTTTGACTATCTTCTCTCTCACTGCTTGGTGGATGGGCAGATCTTCTGTCTACATGGT	686		
566	GGTCTGTCTCCATCGCTCGACACATTTAGATCAATCCGAGCCCTAGATCGTATTTCAAGAA	566	GGTCTGTCTCCATCGCTCGACACATTTAGATCAATCCGAGCCCTAGATCGTATTTCAAGAA	625		
687	GGTCTCTCGGCATCTATAGATACACTGGATCATATCAGAGCAGCTTGATCGCTCAAGAA	687	GGTCTCTCGGCATCTATAGATACACTGGATCATATCAGAGCAGCTTGATCGCTCAAGAA	746		

626	GTCCCGCAGAGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGP	Qy
747	GTTCCTCATGAGGGTCGAATGTGTGACTTGTCTGGTCAGATCCAGATGP	Db
686	TGGGGCATTTCCACCACGAGGTGCCGGTTATACTTTTGGTCAAGATATTGC	Qy
807	TGGGTTATATCTCTCTGAGGAGCTGGTTACACTTTGGCGAAGATATTTT	Db
746	AATCATATCCAAATGCTCTAAGTTTGGTTTGCACGTCTCACCGACTTGTGAM	Qy
867	AATCATGCCAAATGSCCTCACGTTTGGTGTCTAGAGCTCACCGACTAGTGA	Db
806	AATTGGTGCCAGGATAAAATGTTGTGCAGTTTTTCAGTGCCGCCCAATTP	Qy
927	AACGTGTGCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAAACTP	Db
866	TGTGGGAACATGCCGCCCAATAATGGAGATAGATCAACAATGAATCGGTC	Qy
987	TGTGGTAAACCAAGCTGCAATCATGGAACTTTGACCATCTCTAAATACTC	Db
926	TTCGAAACCCAGCACCGCGGCAAGTGAACCCAGATGTGACGCGGAAGACTCC	Qy
1047	TTTGACCCAGCACTCTGTAGAGGCGGCAATGTTACTCTGTCTGTAACCC	Db
986	CTGTAAACATGGCCCTATACATG 1007	Qy
1107	CTGTAAATGAATTTTAAACTTG 1128	Db

```

RESULT 10
US-09-780-049-10
; Sequence 10, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHAT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 10
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(1125)
US-09-780-049-10

```

Query Match 36.1%; Score 493.2; DB 3; Length 17
Best Local Similarity 70.9%; Pred. No. 2.8e-153;
Matches 654; Conservative 0; Mismatches 268; Indels

QY	86	GATGTAGACGGCAGATAGACAGACGCTGTGCGAGTGC	AAAGCCGTTGTTCGG#	TC 145
DB	220	GAGCTGGACAGTGGATCAGACAGCTGAACGAGTGC	AAAGCAGCTCTCCG#	TC 279
QY	146	AAGAACCTTATGTGATCAAGCTCGGACGATCTTGGT	GGAGGAGTGGAAACGT	TC 205
DB	280	AAGAGCCCCGCGAAGGCTAAAGAAATCCTGACAAA	AGAAATCCAAACGT	TT 339
QY	206	AAGTGTCTGTCAACGGTTTGGCGTGACATCCATGG	CCAGCTTTTCATGATCT	TT 265
DB	340	CGATGTCCAGTCACTGTGTGTGAGATGTACATGG	SCAAATTTTCATGATCT	TC 399
QY	266	TTCCGCATAGGAGGCAAGCGCCCGACACGA	ACTTCTTTTATGGGCG#	AT 325
DB	400	TTTAGAAATTTGGTGTAAATCACCAGATACAAA	ATTACCTGTTTATGGGAG#	AC 459
QY	326	CGTGGATATATTCTGTGTGAGACTGTGTCGCTCT	TAGTGGCCCTCGAAGCT	CG 385

ANALYTIC SUBUNIT A


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Db 832 GGTGATGGAGGATATAACTGGTGCCATGACCGAAATGTAGTAACGATTTTCAGTGCTCC 891
Qy 850 CAATTACTGTTACCGCTGGGAACATGCGCCGCATATGGAGATAGATGAACAATGAA 909
Db 892 AAACATATTGTTATCGTTGGTGAACCAAGCTCAATCATGGAACCTGTGATGACTCTAAA 951
Qy 910 TCGGCTTTTCTTCAGTTTCGAACCAAGCACCAGCGGCAAAAGTGAACAGATGTGACGCGGAA 969
Db 952 ATACTCTTTCTTGCAGTTTTCAGCCAGCACC-CGCAGAGCGGAGCCACATGTTACTCGTCG 1010
Qy 970 GACTCTGATTAATTCTCTGTAACATGGCCTATACATG 1007
Db 1011 TACCCAGACTACTTCTCTGTAATGAATTTTAAACTTG 1048

RESULT 12
US-09-828-302-3
; Sequence 3, Application US/09828302
; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-3

Query Match 31.3%; Score 427.6; DB 3; Length 447;
Best Local Similarity 98.9%; Pred. No. 8.7e-132;
Matches 441; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 459 GCCTCGGAAAGTATGGAATGGAATGTTTGAAGTACTTTCAGCGATCTGTTTCGACTACC 518
Db 2 GCACAGAGAGTATGGAATGGAATGTTTGAAGTACTTTCAGCGATCTGTTTCGACTACC 61
Qy 519 TGCCTCTGACAGCTCTCATTTGAGCAGAGATTTTTTGTCTTCATGGTGGTCTGTCTCCAT 578
Db 62 TGCCTCTGACAGCTCTCATTTGAGCAGAGATTTTTTGTCTTCATGGTGGTCTGTCTCCAT 121
Qy 579 CGCTCGACACATTAGATCATATCCAGCGCTTAGCTGTTTCAAGAGTGGCGGACGAGG 638
Db 122 CGCTCGACACATTAGATCATATCCAGCGCTTAGCTGTTTCAAGAGTGGCGGACGAGG 181
Qy 639 GCGCCATGTGTGATCTACTCTGTCTGATCCAGATGATGTTTGTGATGGGCGCATTTTCCAC 698
Db 182 GCGCCATGTGTGATCTACTCTGTCTGATCCAGATGATGTTTGTGATGGGCGCATTTTCCAC 241
Qy 699 CACGAGGTGCGGTTTATCTTTTGGTCAAGATATTGACAGAGCAGTTCAATCATACCAATG 758
Db 242 CACGAGGTGCGGTTTATCTTTTGGTCAAGATATTGACAGAGCAGTTCAATCATACCAATG 301
Qy 759 GTCTAAGTTTGGTTCAGCTGCTACAGCTTGTGATGGAAGGATACAAATTTGGTCCGAGG 818
Db 302 GTCTAAGTTTGGTTCAGCTGCTACAGCTTGTGATGGAAGGATACAAATTTGGTCCGAGG 361
Qy 819 ATAAAAATGTTGTACAGTTTTTCACTGCTGCGCCCAATTTACTGTTTACCGCTGTGGGACATGG 878
Db 362 ATAAAAATGTTGTACAGTTTTTCACTGCTGCGCCCAATTTACTGTTTACCGCTGTGGGACATGG 421
Qy 879 CCGCCATAAT-GGAGATAGATGAAC 903
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Db 422 CGCCCATATGGAGATAGATGAAC 447

RESULT 13
US-09-487-558B-269
; Sequence 269, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Calli, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolit
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 269
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-269

Query Match 30.9%; Score 422; DB 3; Length 1134
Best Local Similarity 66.7%; Pred. No. 1.2e-129;
Matches 602; Conservative 0; Mismatches 300; Indels 3 0;

Qy 90 TAGACCGCAGATAGAGCAGCTGTGCGAGTGCAGAGCCGTTGTCGAGTTC 3A 149
Db 233 TTGACCAATGATGAGCATTTGAGTAAATCGAGCCACTATCAGAGAC AC 292
Qy 150 ACCTATGTGATCAAGCTCGGACGATCTTGTGGAGGAGTGGAACTGCAC 3T 209
Db 293 GACTATGTAAATGCGGTGACGCTTGTTCAGTTCGAGAGAAATGTTAA CG 352
Qy 210 GTCTCTGCACGGTTTGGCGTGACATCCATGCGCCAGTTTTCATGATCTCATC CC 269
Db 353 TGCCTGTATACCATTTGTGTGACGTACACGCTCAATTCATGACTTGTTA CA 412
Qy 270 GCATAGAGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGGACTAT TC 329
Db 413 AGATTGTGTGCTTGTCTCTGACCAATTAACCTTTTCATGGTGATTAC AG 472
Qy 330 GATATTATCTGTGAGACTGTGTGCTTCTAGTGGCCCTGAAGTGGCGG GA 389
Db 473 GATATTATCTGTGAGACCGTATCTTACCTAGTGTGCCATGAAAGTCAGP TA 532
Qy 390 GGATCACAATCTTGCAGGGAACCAACAGAGAGCAGCAGATTACGCAAGT? CT 449
Db 533 GAATTACTATATCTTAGGGCAATCACGAGTCTAGGAGATTACCCAGT? TT 592
Qy 450 ATGATGAATGCTCGGGAAGTATGGAATGGAATGTTTGGAACTACTTC 3T 509
Db 593 ATGACGAATGTTTGAGAAAGTACGCGAGTGCAGACGTTGTGGAATAATGTT AT 652
Qy 510 TCGACTACCTCTCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTT TC 569
Db 653 TCGATTATTTCCCGCTTACTGCTTGTGGGATAATAAAATCTTCTGTTTC TC 712
Qy 570 TGTCTCCATCTCTCGACACATTTAGATCACATCCGAGCCCTAGATCGTATT 3C 629
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tion in : ngi

Db 713 TCTACCCATGATAGAGCAATAGATCAAGTTAGAGATTAAATAGAAATACAGGAAGTGC 772
Qy 630 CGCAGAGGCGCGATGTGTGATCTACTCTGTCTGTATCCAGATGATCGTTGTGTGATGGG 689
Db 773 CTCAGAGGTCCAATGTGTGACCTTCTATGTCGATCCTGATGATAGAGCGGATGGG 832
Qy 690 GAATTTACCAAGAGGTGCGGTTTATACCTTTTGGTCAAGATATTCAGAGCAAGTTCAATC 749
Db 833 GAATCAGTCCGAGAGGTGCGGCTTCACTTTTGGTCAAGACATCAGTGAAGCAATTTCAATC 892
Qy 750 ATACCAATGGTCTAGTTTGGTTCAGCTGCTCACCAGCTTGTGATGGAAGATACAATTT 809
Db 893 ACACAAATGACCTATCACTAATAGCAAGAGCTCACCAATTTGTAATGGAAGATATTTCTT 952
Qy 810 GGTGCCAGGATAAAATGTTGTCACAGTTTTCAGTGCCCCCAATTTACTGTTTACCGCTGTG 869
Db 953 GGTCTCACCAGCAAAATGTTGTCAACATTTTCAGTGCTCCAAATTTATGTTATAGATGTG 1012
Qy 870 GGAAATGCGCGCCCAATATGAGATAGATGAACAAATGAATCGGTCTTTTCTTCAAGTTGG 929
Db 1013 GTAACCGAGCGCTATTATGAGAGGTGGATGAAACCAATAATAGGCAATTTCTTACAATACG 1072
Qy 930 RACCAGCACCGCGCAAGAGTGAACAGATGTGACGCGGAAGACTCCTGATTTACTTTCTGT 989
Db 1073 ATCCATCTGTGAGACCCGGTGAACCAACCGTCAACGGAAGACACCGGATTTATTTCTTAT 1132
Qy 990 AA 991
Db 1133 AA 1134

RESULT 14
US-09-614-221A-47
; Sequence 47, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614, 221A
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 47
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-47

Query Match 29.6%; Score 404.4; DB 3; Length 1110;
Best Local Similarity 65.5%; Pred. No. 8.7e-124;
Matches 591; Conservative 0; Mismatches 311; Indels 0; Gaps 0;
Qy 90 TAGACCGGCAGATAGACAGCTGTGCGAGTGAAGCCGTTGTCGAGTTGGAGGTGAAGA 149
Db 209 TTGACCAATGGATTGAGCATTTGAGTAAATGCGAGCCACTATCAGNAGACGATGTAGCAC 268
Qy 150 ACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGAGTGGAAACGTCGAGCCCGTGAAGT 209
Db 269 GACTATGTAATAATGGCGGTGGACGTTGTCAGTTTCAGGAGAAATGTTAAACCAATTAACG 328
Qy 210 GTCTGTGACGGTTTGGGTGACATCCATGCGCAGTTTTCATGATCTCATCGAGCTTTCC 269
Db 329 TGCCGTGTACCAATTTTGGTGGTACGTCACGGTCAATTTCCATGCTGTTAGAACATTTTAA 388
Qy 270 GCATAGGAGGCAAGGCGCCGACGACGAACTACTTGTTCATGGCGCACTATGTGGATCGTG 329
Db 389 AGATTGGTGGCCCTTGTCTGACACCAATTACTTTTTCATGGTGTGATTACGTGGATAGAG 448

Qy 330 GATATTATTTCTGTGAGACTGTGTGCGCTCTTTAGTGGGCCCTGAAAGTGGCGG' A 389
Db 449 GATATTATTTCTGTGTTGAAAACCTGTATCTTTACCTAGTTGGCCATGAAAAGTCAGA' A 508
Qy 390 GGATCACAATCTTCGCGAGGGAACACGAGAGACGCGCAGATTACGCAAGTA' T 449
Db 509 GAATTTACGATCTGAGAGGCAATCAGAGTCTAGGCAGATTACCCAAAGTA' T 568
Qy 450 ATGATGAATGCTCGGGAAGTATGGAATGCGAATGTTTGGAAAGTACTTTC. T 509
Db 569 ATGATGAATGTTTGGAAAAGTACGCGAGTCAACGCTGTGGAAAATGTTTC. T 628
Qy 510 TCGACTTACCTGCTCTGACAGCTCTCATTTGAGCAGAGATTTTTTTGTCTTT' C 569
Db 629 TCGATTATTTTCTTATAACCGCATTTAGTAGATAATAAAATTTTCTGTCTG' C 688
Qy 570 TGTCTCCATGCTCGACACATTTAGATCACATCCGAGCCCTAGATCGTATT' C 629
Db 689 TTTCCCCCATGATAGAAACCATAGATCAGGTGAGAGAGTTGAAACAGAATA' C 748
Qy 630 CGCAGAGGCGCGGATGTGTGATCTACTCTGCTGTGATCTTGTGATCCAGATGATCGT' G 689
Db 749 CTGATGAAGTCTTATGTGTGACCTTCTATGTTGTCAGACCTTGAACCGATAGA' G 808
Qy 690 GCATTTCAACGAGGTGCGGTTTATCTTTTGGTCAAGATATTGCCAGAG' C 749
Db 809 GAATCAGTCCGAGAGGTGCGGCTTCACTTTTGGACAAGATGTCTAGTGAG' C 868
Qy 750 ATACCAATGGTCTAAGTTTGGTGTGACGCTGTCCAGCTCTTGTGTGATGGA' T 809
Db 869 ACATTAATGATCTATCACTAATAGCAAGAGCTCAACAAATTTGGTAATGGA' T 928
Qy 810 GGTGCCAGGATAAAAAATGTTGTCAAGTTTTCAGTGTGCCCCCAATTTACTGT' G 869
Db 929 GGTCTCACCAGCAAAAATGTTGTCAACCAATTTTTCAGTGTCTCTTAATTTACTGC' G 988
Qy 870 GGAACATGCGCGCCCATATATGAGATAGATGAAACAAATGAATCGGTCTTTT' G 929
Db 989 GTAATCAAGAGCTATCATGGAAGTGGACGAGAATCATATAAGACAATTC' G 1048
Qy 930 AACCAGCACCGCGCAAAAGTGAACAGATGTGACGCGGAAGACTCCTGTAT' T 989
Db 1049 ACCATCGTGAAGACCGGTGAACCTAGCGTCAAGCAAGAACGCCAGAT' T 1108
Qy 990 AA 991
Db 1109 GA 1110

RESULT 15
US-09-487-558B-267
; Sequence 267, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolit
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487, 558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487, 558

;
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 267
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-267

Query Match 29.6%; Score 404.4; DB 3; Length 1110;
Best Local Similarity 65.5%; Pred. No. 8.7e-124; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 311;
QY 90 TAGACGGCAGATAGACGAGCTGTGGAGTGAAGCCGTTGCGAGTTGGAGGTGAAGA 149
Db |||||
QY 209 TTGACCAATGGATTGAGCAATTTGAGTAAATGCGAGCCACTATCAGAAGACGATGTAGCAC 268
Db |||||
QY 150 ACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGAGTGGAACTGCGAGCCCGTGAAGT 209
Db |||||
QY 269 GACTATGTAAATGGCGGTGGACGTTTGCAGTTCGAGGAGAACTGTTAAACCAATTAACG 328
Db |||||
QY 210 GTCTGTCAAGCTTTGCGGTGACATCCATGCGCAGTTTTCATGATCTCATCGAGCTTTTCC 269
Db |||||
QY 329 TGCCCTGTTACCAATTTGTTGGTGAAGTACACGGTCAATTCATGACTTGTAGAACTTTTA 388
Db |||||
QY 270 GCATAGGAGGCAAGGCCGCCGACGAACTACTTGTTCATGGCGACTATGTGGATCGTG 329
Db |||||
QY 389 AGATTGGTGGCCCTTGTCTCGACACCAATTTACCTTTTCATGGTGTATACGTGGATAGAG 448
Db |||||
QY 330 GATATATATCTGTCAGACTGTGTGCTCTAGTGGCCCTGAAGTGGCGGTATAGGGATA 389
Db |||||
QY 449 GATATATATCTGTTGAAACTGTATCTTACCTAGTTGCCATGAAAGTCAAGTACCCACATA 508
Db |||||
QY 390 GGATCACAACTCTGCGAGGGAACACGAGAGCAGAGGACGAGTACGCAAGTATATGTTCT 449
Db |||||
QY 509 GAATTTACGATCTGAGAGGCAATCAGAGTCTAGGAGATACCCAAAGTATACGGGTTTT 568
Db |||||
QY 450 ATGATGAATGCTCGGAGTATGGAATGCGAATGTTTGGAACTACTTCAAGGATCTGT 509
Db |||||
QY 569 ATGATGAATGTTTGAGAAAGTACGCGAGTGCACAACTGTGGAAATGTTCAAGATCTTT 628
Db |||||
QY 510 TCGACTACCTGCTCTGACAGCTCTCACTTGGACGACGAGATTTTGTCTTATGTGTGTC 569
Db |||||
QY 629 TCGATTATTTTCTTAACCGCATTTAGTAGATAATAAAATTTTCTGTCTGCATGGAGAC 688
Db |||||
QY 570 TGCTCTCCATCGCTCGACATTTAGATACATCCGAGCCCTAGATCGTATTCAGAGAGTGC 629
Db |||||
QY 689 TTTCCCAATGATAGAAACCATAGATCAGGTGAGAGAGTTGAACAGAAATACAGGAAGTGC 748
Db |||||
QY 630 CGCAGAGGCGCGGATGTGTGATCTACTCTGTCTGATCCAGATGATCGTTGTGGATGGG 689
Db |||||
QY 749 CTCATGAAGTCTTATGTGTGACCTTCTATGTGTGACCTGACCTGACGTAGAGCGGATGGG 808
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Db |||||
QY 750 ATACCAATGTCTAAGTTTGGTGGACGTCTCACCAGCTTGTGATGGAGGATACAAAT 809
Db |||||
QY 869 ACATTAATGATCTATCATTAATAGCAAGAGCTCACCAATGGTAAATGGAAGGCTATGCTT 928
Db |||||
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Db |||||
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Db |||||
QY 930 AACAGCAGCGCGCAAGTGAACAGATGTGACCGGAGAGCTCTCTGATTTCTTCTGT 989
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Db |||||

QY 990 AA 991
Db 1109 GA 1110

Search completed: December 9, 2005, 09:55:30
Job time : 283 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 06:30:04 ; Search time 1078 Seconds
(without alignments)
10470.966 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggaggag.....tatggcatgctcgagctgc 1365

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1365	100.0	1365	3	US-09-828-302-8
2	1365	100.0	1365	7	US-10-764-259-8
3	596.6	43.7	1732	7	US-10-425-114-35277
4	592	43.4	1525	8	US-10-425-115-160542
5	589.6	43.2	1386	6	US-10-236-699-21
6	584	42.8	1330	6	US-10-236-699-31
7	582.8	42.7	1298	6	US-10-236-699-25
8	579.8	42.5	1195	7	US-10-437-963-40723
9	559.4	41.0	921	3	US-09-938-842A-705
10	559.4	41.0	921	3	US-09-938-842A-705
11	556.6	40.8	1879	8	US-10-425-115-149113
12	552.8	40.5	1243	6	US-10-236-699-7
13	547.6	40.1	1761	7	US-10-424-599-20866
14	531.8	39.0	924	3	US-09-938-842A-571
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17	517.4	37.9	1487	7	US-10-236-699-23
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19	514	37.7	1279	6	US-10-236-699-2
20	514	37.7	1531	6	US-10-210-120-42
21	514	37.7	1531	9	US-10-909-035-42
22	512.4	37.5	1529	3	US-09-880-107-2098
23	512.4	37.5	1541	9	US-10-956-157-1198

24	510.2	37.4	1580	6	US-10-388-934-575	Seq
25	510.2	37.4	1843	3	US-09-917-800A-1625	Seq
26	510.2	37.4	1843	7	US-10-191-803-84	Seq
27	510.2	37.4	1843	7	US-10-152-319A-1641	Seq
28	510.2	37.4	1843	7	US-10-467-008-10	Seq
29	507.6	37.2	1804	3	US-09-917-800A-1624	Seq
30	507.6	37.2	1804	7	US-10-191-803-83	Seq
31	507.6	37.2	1804	9	US-10-386-971-2	Seq
32	506	37.1	1738	6	US-10-388-934-574	Seq
33	505.2	37.0	2181	6	US-10-007-926A-184	Seq
34	505.2	37.0	2181	6	US-10-467-126-17	Seq
35	505.2	37.0	2181	9	US-10-936-273-20	Seq
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37	501.4	36.7	1798	8	US-10-425-115-103273	Seq
38	501.2	36.7	1787	6	US-10-291-808-39	Seq
39	499	36.6	1716	7	US-10-424-599-24013	Seq
40	498.2	36.5	1576	7	US-10-425-114-32875	Seq
41	498.2	36.5	1822	7	US-10-425-114-3464	Seq
42	498.2	36.5	2209	8	US-10-425-115-102388	Seq
43	496.2	36.4	2086	7	US-10-425-114-35289	Seq
44	493.6	36.2	1587	6	US-10-236-699-17	Seq
45	493.2	36.1	1781	7	US-10-467-126-10	Seq

ALIGNMENTS

RESULT 1

US-09-828-302-8

; Sequence 8, Application US/09828302

; Patent No. US20020152502A1

; GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, ROUYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N

; FILE REFERENCE: 16313-0029

; CURRENT APPLICATION NUMBER: US/09/828,302

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 1365

; TYPE: DNA

; ORGANISM: Physcomitrella patens

US-09-828-302-8

Query Match	100.0%	Score 1365;	DB 3;	Length 13
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1365;	Conservative 0;	Mismatches 0;		
Indels				
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Db	1	GGCGTTAAACCGCGGAGGAGCGGATCGGTTAGCGTTTGGTTCAGGGG	3A 60	
Qy	61	GGTTGGGACATCGCGTCATATGCAGATGTAGACCGGCAGATAGACGAC	1G 120	
Db	61	GGTTGGGACATCGCGTCATATGCAGATGTAGACCGGCAGATAGACGAC	1G 120	
Qy	121	CAACCGGTTTCGAGTTGGAGTGAAGAACTATGTATCAAGTCGGA	3T 180	
Db	121	CAACCGGTTTCGAGTTGGAGTGAAGAACTATGTATCAAGTCGGA	3T 180	
Qy	181	GGAGGAGTGAACCTGCAGCCCGGGAAGTGTCCTGTCACCGTTTGGCGTG	3G 240	
Db	181	GGAGGAGTGAACCTGCAGCCCGGGAAGTGTCCTGTCACCGTTTGGCGTG	3G 240	
Qy	241	CCAGTTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGGCAAGCGCCCG	TA 300	
Db	241	CCAGTTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGGCAAGCGCCCG	TA 300	

Db 241 CCAGTTTCATGATCTCATCGAGCTTTTCGCGATAGGAGCAAGGCCCGCAGACGACTA 300
QY 301 CTTGTTTCATGGCGGCGACTATGGGATCGGTGGATPATTATTTCTGTCGAGACTGTGTCGCTTT 360
Db 301 CTTGTTTCATGGCGGCGACTATGGGATCGGTGGATPATTATTTCTGTCGAGACTGTGTCGCTTT 360
QY 361 AGTGGCCCTGAGGTCGGGTATAGGATAGGATCACAATCTTTCGAGGAACCCAGAGAG 420
Db 361 AGTGGCCCTGAGGTCGGGTATAGGATAGGATCACAATCTTTCGAGGAACCCAGAGAG 420
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QY 481 GAATGTTTGGAAAGTACTTCACGGATCTGTTTCGACTACCTGCTCTGACGCTCTCAATTGA 540
Db 481 GAATGTTTGGAAAGTACTTCACGGATCTGTTTCGACTACCTGCTCTGACGCTCTCAATTGA 540
QY 541 GCACGAGATTTTTTCTCTTCATGTTGGTGGTCTGTTCTCCATCGCTCGACATTAGATCACAT 600
Db 541 GCACGAGATTTTTTCTCTTCATGTTGGTGGTCTGTTCTCCATCGCTCGACATTAGATCACAT 600
QY 601 CGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGAGGCCCGATGTGTGATCTACTCTG 660
Db 601 CGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGAGGCCCGATGTGTGATCTACTCTG 660
QY 661 GTCTGATCCAGATGATCGTTGGATGGGCAATTTCAACAGAGTGCCGTTTACATTT 720
Db 661 GTCTGATCCAGATGATCGTTGGATGGGCAATTTCAACAGAGTGCCGTTTACATTT 720
QY 721 TGGTCAAGATATTGAGAGCAGTCAATCATACCAATGGTCTAACTTTGGTTCGACGTGC 780
Db 721 TGGTCAAGATATTGAGAGCAGTCAATCATACCAATGGTCTAACTTTGGTTCGACGTGC 780
QY 781 TCACCACTGTTGATGGGAAGGATACAAATGGTGCCAGGATAAAATGTTGTACAGATTTT 840
Db 781 TCACCACTGTTGATGGGAAGGATACAAATGGTGCCAGGATAAAATGTTGTACAGATTTT 840
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Db 841 CAGTGCCTCCCAATTAATCTGTTACCGTGTGGGAACATGCGCCGCAATAATGGAGATAGTGA 900
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Db 901 AACATGAATCGTCTTTCTTCAGTTCGAAACAGCAGCCGCGGCAAGTGAACAGATGT 960
QY 961 GACGCGGAAGACTCTCTGATTAATCTTCTGTAAACATGGCCTATACATGTTACCTTTACTT 1020
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QY 1021 ACTGAATGTTCTGTATAGTCACTTCCATGGAAGCAGTTGCCCCTGAATGAAGATACT 1080
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QY 1081 CCCTCATGATCTAGTAGTGAAGTATCTTCTTTGAAAGTGTGTTCCCTTTTATGTA 1140
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Db 1321 AACGTTCTATCTCCACACCTACTGTATATGGCATGTCTCGAGCTCGC 1365

RESULT 2
US-10-764-259-8
; Sequence 8, Application US/10764259
; Publication No. US20040148658A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND M
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/10/764,259
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-764-259-8

Query Match 100.0%; Score 1365; DB 7; Length 13.
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 0; Indels 0;
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Db 1 GGCCTTAACCGCGGAGGAGCGGATCGGTAGGTTTGGTGCAGGGG 60
QY 61 GGTGGGACATGCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 120
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QY 181 GGAGGAGTGGAACTGCGAGCCGCTGAGTGTCTGTCACGGTTTGCCTG 240
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QY 301 CTTGTTTCATGGGCGACTATGTGGATCGGTGGATATTTATTTCTGTCGAGACTG 360
Db 301 CTTGTTTCATGGGCGACTATGTGGATCGGTGGATATTTATTTCTGTCGAGACTG 360
QY 361 AGTGGCCCTGAGGTCGGGTATAGGATAGGATCACAATCTTTCGAGGGA 420
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QY 421 CAGGCAGATTACCGCAAGTATATGGTTTCTATGATGAATGCCCTCGCGAAGT 480
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Db 781 TCACAGCTTTGTGATGGAAGGATACAAATTTGGTCCAGGATAAAATGTTGTCCACAGTTT 840
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Db 841 CAGTCCGCCCAATTAATCTGTTACCGCTGTGGGAACATGCGCCCATATAATGGAGATAGATGA 900
Qy 901 AACATGAATCGGCTCTTTCTTTCAGTTGGAACAGACACCGCGGCAAAAGTGAACAGATGT 960
Db 901 AACATGAATCGGCTCTTTCTTTCAGTTGGAACAGACACCGCGGCAAAAGTGAACAGATGT 960
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Db 961 GACGCGGAAGACTCTCGATTAATCTTCTGTAACATGGGCTATACATGGTACCTTTTACTT 1020
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Db 1201 CTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGTTTATAGTATAGGGAAGAGGT 1260
Qy 1261 AGCAGATGTTACTTCAATTCAGATCAGAGACTTCTATGGAAGATGACGATGGTGAAC 1320
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Db 1321 AACGTTTCTCTCCACCTACTGTATATGGCATGCTCGAGCTCGC 1365

RESULT 3
US-10-425-114-35277
; Sequence 35277, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; INVENTION FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35277
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE90H04_FLI

US-10-425-114-35277

Query Match 43.7%; Score 596.6; DB 7; Length 17
Best Local Similarity 76.9%; Pred. No. 2.9e-181;
Matches 728; Conservative 0; Mismatches 219; Indels
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Qy 108 AGCTGTCCGAGTGCAGCCGTTTCGGAGTTGGAGGTGAAGAACCTATGT 3C 258
Db 259 AGCTGCGGGATTGCAAGTTCTTCCGCGAGGTGAGGTCAAGACGCTATGC 1C 167
Qy 168 GGACCATCTTGGTGGAGAGTGGAACTGCGAGCCGTTGAAGTGTCTCTGTC 1A 318
Db 319 AGGCGATCTCATGAGAGGTGGAACTGCGAGCCGTTGGCTGCCCGGTC 3G 227
Qy 228 GTGACATCCATGGCCAGTTTTCATGATCTCATCGAGCTTTTCGGCATAGGA 3G 378
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Qy 288 CCGACACGAACACTTGTGTCATGGCGGACTATGCGATCGTGATATTAT 3C 438
Db 439 CAGACACCAACTTACCTCTTTATGGCGGATTACGTCGACCGTGGCTACTAC 3A 347
Qy 348 CTGTGTGCTCTTGTAGTGGCCCTGGAAGTGGCGTATAGGATAGGATCACT 3A 498
Db 499 CTGTGTGCTTGTGTAGTGGCTCTTAAAGTACGTTTATAGAGACAGATCACT 1G 407
Qy 408 GGAACCCAGAGCAGGAGGATTAACGCAAGTATATGGTTCTATGATGAT 1G 558
Db 559 GAAATCATGAGAGCAGACAAATACTCAAGTGTATGGCTTCTATGATGAT 3A 467
Qy 468 AGTATGGAATGCGAATGTTTGGAACTTCTTCAAGTCTGTCGACTAC 3A 618
Db 619 AATATGGAATGCAAAATGTTGGAAGTACTTTACAGACTTGTGTTGATTA 3A 527
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Db 679 CAGCTCTTATGAAAACAGATCTTCTGCTTACATGGTGGTCTCTCTCP 2A 587
Qy 588 CATTAGATCAGATCCGAGCCCTAGATCGTATTTCAAGAAAGTCCCGCAGAG 1A 738
Db 739 CATTGGAATAATCCGCGCCCTTGATCGCATACAAGAGGTCCCATCATGAT 3T 647
Qy 648 GTGATCTACTCTGTCTGATCCAGATGATGTTGGATGGGCAATTTCTP 3T 798
Db 799 GTGATCTTTTGTGGTCTGACCCAGATGACCGATGTTGGGTGGGAAATTTCT 1G 707
Qy 708 CCGGTTATACTTTTGGTCAAGATATGCGAGAGCTTCAATCATACCAAT 1G 858
Db 859 CTGGATACAAATTTGGCCCAAGATATGCGAACAAATTCACCATACAAAT 1T 767
Qy 768 TGGTTGCAAGTGTCTCACCCAGCTTGTGATGGAAGGATACAATTTGGTGGCAG 1C 918
Db 919 TTAATTTCAAGGGCAGATCACTTGTATGGAAGGCTTCAATTTGGTGTCA 1G 827
Qy 828 TTGTCACAGTTTTCAGTGGCCCCCAATTAATCTGTTACCGCTGTGGGAACATC 1G 978
Db 979 TTGTGACTGTGTTTCAGCGCGCTTAATCTACTGCTACCGATGCGGAACATC 1A 887
Qy 888 TGGAGATAGTAAGAACATGAATGATCGTCTTCTTCTTCAAGTTCGAAACAGCA 3C 1038
Db 1039 TCGAAATTTGGCGAGAACATGATCAGAACTTCTCTCAATTCGACCCAGCT 1A 947
Qy 948 GTGAACACAGATGTGACCGCGGAGAGCTCTCTGATTAATTTCTCTGTAAACA 1A 1098
Db 1099 TTGAGCCGACATGACCGCGCAAGACACCCAGACTACTTTTGTAGAAA 11

RESULT 4
US-10-425-115-160542

380 TATAGGATAGGATCAATCTTGGAGGAAACACGAGAGCAGGACAGATTACGCAAGTA 439
401 TATAGAGATAGATCAATCTTCAAGGGAATCATGAAGCCGTCAAATTAATCAAGTG 460
440 TATGTTCTTATGATGAATGCTCGGAGATGAAATGCAATGTTTGGAAAGTACTTC 499
461 TATGCTCTTATGATGAATGCTTGAAGAAATATGGAATGCAATGCTGGAATATCTT 520
500 ACGGATCTTTCAGTACTGCTCTGACAGCTCTCATTTGACGACAGATTTTGTCTT 559
521 ACAGACTTGTITGATATTTGCTCTGACTGCTCCCTCATTTGAGATGACAGATTTTCTGCTG 580
560 CATGTTGTTCTGCTCTCTGCTGCTGACACATTTAGATCAATCCGAGCCCTAGATCGTATT 619
581 CATGAGGTCTCTACCTCTTTTGGATACATGATTAACATCAGAGCATTTGATCGTATT 640
620 CAAGAGTCCGACAGAGCCGATGTTGATCTACTCTGCTCTGATCCAGATGATCGT 679
641 CAAGAGGTTCACATGAAGGACCAATGTTGATCTCTTGTGCTCTGACCCCTGATGATGCG 700
680 TGTGATGCGGATTTTCCACGAGGTGCGGTTATCTTTTGGTCAAGATATTCAGAG 739
701 TGTGATGCGGATATCTCCAGTGGTGAGGATACATTTTGGGAGGATATAGCTGCT 760
740 CAGTTCAATATACCAATGGTCTAAAGTTTGGTTCACGCTGCTCACAGCTTGTGATGAA 799
761 CAGTTTATATACCAATGGCTCTCCCTGATATCAGAGCATCATCAGTGTGATGAA 820
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821 GGATTTCAATTTGTCAGAGATTAATGTTGTCAGATTTTCAAGTTCGAGTCCCAATTAATCTGT 880
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920 CTTCAAGTTTCAAGTCCAGTCCAGGCAATTTGAGCTTGACACACACGAGACTCTCTGAT 979
941 CTTCAAGTTTCAAGTCCAGTCCAGGCAATTTGAGCTTGACACACACGAGACTCTCTGAT 991
980 TACTTTCTGTAA 991
1001 TATTTTGTAA 1012

RESULT 6
US-10-236-699-31
; Sequence 31, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-31

Query Match 42.8%; Score 584; DB 6; Length 1330;
Best Local Similarity 76.2%; Pred. No. 2.9e-177;

Matches 719; Conservative 0; Mismatches 225; Indels
QY 48 GGGGGAGGGCAGAGGTTGGGCAATGCGCTCATATGCGAGATGTACACCG 0;
DB 81 GGAGGTGGGAGCGAAACGAAACGATGCGCTCTCACGGGATCTGGAACG# 3C 107
QY 108 AGCTGTCCGAGTGCAAGCCGTTGTCGAGTGGAGGTGAAGAACCTATGT 3C 140
DB 141 AGCTGATGAGTGCAAGCCCTCTGTCGAGTGGAGTGAAGCGCTGTGT 3C 167
QY 168 GGACGATCTTGGTGGAGGAGTGGAACGTCGAGCCGTCGAGTGTCTGT 3A 200
DB 201 GGGCGATTTCTGTCGAGGAATGGAACGTCGAACCGGTGAAGTGCCTGTC 3G 227
QY 228 GTGACATCCATGGCCAGTTTCATGATCTCATCGAGCTTTTCGCGATAG# 3G 260
DB 261 GCGATATTTCAGCGCCAGTTTACGATCTCATCGAGCTGTTTCGGATGGA 3C 287
QY 288 CCGACACGAATCTACTTGTTCATGGCGCACTATGTGGATCGTGGATATTAT 3C 320
DB 321 CCGATACCAATTAATCTCTTTCATGGGTGATTATGATCGTGGATATTAT 3A 347
QY 348 CTGTGCTCTTATGTCGCCCTGAAAGTGGCGGTATAGGATAGGATACAT 3A 380
DB 381 CTGTTACACTTTTGGTGGCTTTGAAAGTCCGTTACAGAGATAGATCACA 3G 407
QY 408 GGAACCCAGAGCAGGAGGATACGCAAGTATATGTTTCTATGATGAA 3A 467
DB 441 GAAATCATGAAGTCTGCAAAATTAATCAAGTGTATGGCTTCTATGATGA 3A 500
QY 468 AGTATGGAATTCGAAATGTTTGGAAAGTACTTTCAGCGATCTGTTGCTAC 3A 527
DB 501 AATATGGAATTCGCAATGCTCTGGAATTAATTTACAGACTTGTGTTGATTAT 3A 560
QY 528 CAGCTCTCATTTGAGCAGAGATTTTGTCTCTCATGTTGGTGTCTGTCTCP 3A 587
DB 561 CTGCCCTCATTTGAGAGTCAAGATTTTCTGTTGCTGAGAGGTCTCTCACT 3A 620
QY 588 CATTAGATCATATCCGAGCCCTAGATCGTATTCAGAGAGTCCGCGACGAC 3T 647
DB 621 CACTGGATAACATCAGAGCATTTGGATCGTATACAGAGGTCCCATGAT 3T 680
QY 648 GTGATCTACTCTGCTCTGATCCAGATGATCTGTTGATGGGCAATTTCTP 3G 707
DB 681 GTGATCTCTGCTGCTGACCCCTGATGATCGCTGTTGGATGGGATATCT 3G 740
QY 708 CCGTTATATCTTTTGGTCAAGATATTCAGAGAGTTCATCATACCAAT 3T 767
DB 741 CAGGATACATTTTGGACAGGATATAGCTGCTCAGTTTAAATCATACCAAT 3C 800
QY 768 TGGTTGACAGTCTGCTCACCGCTTGTGATGGAGGATACAAATTTGGTCCAC 3G 827
DB 801 TGATATCAGAGCTCATCAGCTTGTATGGAAGGATTCAAATTTGGTGGCAC 3G 860
QY 828 TTGTCACAGTTTTCAGTGGCCCCCAATTAATCTGTTACCGCTGTGGGAACATC 3A 887
DB 861 TGGTGACTGTATTAGTGCACCAATTAATCTGTTACCGATGTGGGATATC 3C 920
QY 888 TGGAGATAGATGAACCAATGAATCGGTCTTTTCTTCAAGTTCGAAACGAT 3A 947
DB 921 TAGAAATAGGAGAGAAATATGATGATCAGAAATTTCTTCAAGTTCGAGCG 3A 980
QY 948 GTGAACAGATGTGACCGGAGAGTCTCTGATTTCTTCTGTAA 991
DB 981 TTGAGCTGTGACACACGAGCAAGTCTCAGATTTATTTTATAA 1024

RESULT 7
US-10-236-699-25
; Sequence 25, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING		
; APPLICANT: ISHITANI, MANABU		
; APPLICANT: VAN THIELEN, NOCHA		
; APPLICANT: COSTA E SILVA, OSWALDO DA		
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND		
; TITLE OF INVENTION: METHODS OF USE IN PLANTS		
; FILE REFERENCE: 16313-0161		
; CURRENT APPLICATION NUMBER: US/10/236,699		
; CURRENT FILING DATE: 2002-09-05		
; PRIOR APPLICATION NUMBER: 60/317,305		
; PRIOR FILING DATE: 2001-09-05		
; NUMBER OF SEQ ID NOS: 43		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 25		
; LENGTH: 1298		
; TYPE: DNA		
; ORGANISM: Oryza sativa		
US-10-236-699-25		
Query Match 42.7%; Score 582.8; DB 6; Length 1298;		
Best Local Similarity 76.3%; Pred. No. 7.1e-177;		
Matches 716; Conservative 0; Mismatches 222; Indels 0; Gaps 0;		
Qy	54	GGG CAGAGGTTGGGACAAATGCCGTCAATATGCAGATGTAGACCGGCAGATAGAGCAGCTGT 113
Db	159	GTGGGGGAGAGGATGCCGTGTCGACAGGGGATCTGGACCGGCAGATCGCGCAGCTGC 218
Qy	114	CGAGTGC AAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGACGA 173
Db	219	GGGAGTGC AAGCACCTCGCGGAGGGGAGGTGAGGGCGCTGTGCGAGCAGGCGGAAGGCCA 278
Qy	174	TC TTGGTGGAGGAGTGGAAGCTGCAGCCCGTGAAGTGTCTCTCACCGTTTGCGTGTCACA 233
Db	279	TCCTCATGGAGGAGTGGAAAGTCGCAGCCGCTGCGGTGCCCCGTCAACGTTCTGCGCGACA 338
Qy	234	TCCATGCCCAGTTTCATGATCTCATCGAGCTTTTCGCATAGGAGGCAAGCGCCGCGACA 293
Db	339	TCCACGCCAGTTCTACGACCTCATCGAGCTCTTCCGCATCGGCGCGAGCGCGCCGACA 398
Qy	294	CGA CTA CTTGTTTCATGGGCGCACTATGTGGATCGTGGATATATTCTGTGAGACTGTGT 353
Db	399	CCAAC TACCTCTTCATGGGCGACTACGTGCACCGTGGCTACTACTCAGTGGAGACTGTTT 458
Qy	354	CGCTCTTAGTGGCCCTGAAAGTGGCGGTATAGGGATAGGATCACAATCTTTCGAGGGAAAC 413
Db	459	CGTTGTTGGTCTTGAAAGTACGCTACAGAGATCGAATTTACAATATTGAGAGGAATC 518
Qy	414	ACGAGCAGCGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCTCGCGGAAGTATG 473
Db	519	ATGAGACGACAGAAATCACTCAAGTGTACCGCTTCTACGATGAATGCTTGAGAAAGTATG 578
Qy	474	GAAATGCGAATGTTTGAAGTACTTTCACGGATCTGTTTCGACTACCTGCCTCTGACAGCTC 533
Db	579	GAAATGCAATGATGGAATACATTTTACAGACTTGTTTGATATTATTTGCTCTCACAGCTC 638
Qy	534	TCAATGAGCAGAGATTTTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACACATTAG 593
Db	639	TTATAGAAAAACAGGTGTTCTGCCCTTCACGGTGGTCTCTCTCCATCATTTGGATACCTT 698
Qy	594	ATCACATCCGAGCCCTAGATCGTATTTCAAGNAGTCCGCACGAGGGCCCGATGTGTGATC 653
Db	699	ATAACATCCGTGCTCTTGATCGTATACAAGAGGTTCTCTCATGAAGGCCCATGTGTGATC 758
Qy	654	TACTCTGGTCTGATCCAGATGATCGTTTGTGGATGGGGCAATTTTCAACACGAGGTGCCCG 713
Db	759	TTTTTGTGTC TGACCCAGATGACAGATGCGGGTGGGAAATTTTCAACGAGGAGGACAGTT 818
Qy	714	ATACTTTTGGTCAAGATATTGCAGAGCAGTTCAATCATACAATGTGTTCAAGTTTGGTTG 773
Db	819	ATACATTTGGGCAAGATATCGCTCAACAGTTTAAACCATACAATATGGTCTACTCTCATCT 878
Qy	774	CAGTGCTCACCAAGCTTGTGATGGAAAGGATACAATTTGGTCCGAGGATAAAAATTTGTGCA 833

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QY 493 GATCTTACGGATCTGTTGGACTACCTGCTCTGACAGCTCTCATTTGAGCAGAGATTTT 552
DB 426 ATACTTTACAGACTGTTTGAATATTTGCTCTCAGAGCTCTTAGAAAAACAGAGTGT 485
QY 553 TTGCTCTTCATGCTGCTCTCTCCATCGCTCGACACATAGATCATCCGAGCCCTAGA 612
DB 486 CTGCTCTTACGGTGTCTCTCTCCATCATTTGATATCTTTAGATAACATCCGCTCTTGA 545
QY 613 TCGTATTCAAGAGTCCGCGACAGAGGCGCCGATGTGTATCTCTGCTCTGATCCAGAG 672
DB 546 TCGTATACAGAGGTTCTCTCATGAGGACCCATGTGTATCTTTTGGTCTGACCCAGA 605
QY 673 TGATCGTTGTGATGGGCAATTTACACAGAGGTCGCGGTTATATCTTTTGGTCAAGATAT 732
DB 606 TGACAGATGCGGTCGGGAAATTTCAACAGAGAGGAGGAGTTATACATTTGGGCAAGATAT 665
QY 733 TGCAGACAGATTCATCATACCAATGCTTAAGTTTGGTGTGACAGCTCTCACCAGCTTGT 792
DB 666 CGCTCAACAGTTTAAACCATACCAATGCTTATCTCTCATCTCAAGGGGACATCAACTTGT 725
QY 793 GATGAAGGATACAAATGCTGCGCAGGATAAAATGTTGTCAAGTTCAGTGCCCCCAA 852
DB 726 AATGAAGATTTAATTTGGTGTGACGACAGAAATGTTGTGACGGTCTTCAAGTGACCAA 785
QY 853 TTACTGTTACCGCTGTGGGAACATGCGCGCCCAATAATGGAGATAGATGAACAAATGAATCG 912
DB 786 CTACTGTTATCGCTGTGTAACATGGCTGCAATCTTGGAGATGGCGAAACATGGATCA 845
QY 913 GTCCTTTCTCAGTTCGAACAGACCGCGGCAAGTGAACAGATGTGACCGGAGAC 972
DB 846 GAATTCCTCCAAATTTGATTCAGCTCTCTCGGCAATTTGAACAGACACAACACGCAAGAC 905
QY 973 TCCTGATTACTTCTGTAA 991
DB 906 TCCCGACTACTTTTGTA 924

RESULT 9
US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 705
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-705

Query Match 41.0%; Score 559.4; DB 3; Length 921;
Best Local Similarity 75.5%; Pred. No. 2.1e-169;
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 71 ATGCGCTCATATGAGATGATAGACGGCAGATAGACAGCTGTGCGAGTGTCAAGCCGTTG 130
DB 1 ATGCGTTAAACGGAGATCTGACCGTCAGATCGAACAGCTAATGGAGTGAAGCCGTTA 60

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QY 131 TCGAGTTGGAGTGAAGAACCTATGTGATCAAGCTCGAGCATCTTGGT 390
DB 61 GGTGAAGCAGACGTAAGATCTTTTGGCATCAAGCTAAAGCGATCTTGT 120
QY 191 AACGTGAGCCGCTGAGTGTCTGTGACGGTTCGGGTGACATCCATGC 250
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATGCGGCGATATCCATGC 180
QY 251 GATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCGACACCACTA 310
DB 181 GACCTAATTTGAGCTATTTTCGTATTTGGTGTATGCTCTCTGATCTAATTA 240
QY 311 GCGGACTATGTGATGCGTGTGATATTTCTGTGAGACTGTGTGCTCTT 370
DB 241 GGAGATTTATGATAGTGTGCTGTCTATTTCTGTAGAAAACAGTCTCTCTATT 300
QY 371 AAGTGGCGTATAGGATAGGATCACATCTTTGCGAGGGAACCGAGAC 430
DB 301 AAGTGGCGTATACAGGACAGACTTACGATCTCTGAGGGAATCATGAGAC 360
QY 431 ACGAAGTATATGTTTCTATGATGAATGCTCGGAAAGTATGGAATGC 490
DB 361 ACACAGTCTATGTTTATGACGAATGCTTGAGAAATACGGAATGC 420
QY 491 AAGTACTTCAAGGATCTGTGACTTCTGACTGACAGCTCTCATTTG 550
DB 421 AAGTATTTTACGAGACCTTTTTCGATTTCTCTCTCTTACAGCATCATAG 480
QY 551 TTTTGTCTTCTGATGCTGTCTCTCCATGCTCGACACATAGATCAAT 610
DB 481 TTCTGTTTGGATGAGGCTTTTTCACCTTCTCTGATCTCTTGAACATAT 540
QY 611 GATCGTATTTCAAGAGTGCAGGCGCCGATGCTGATCTACTCTG 670
DB 541 GATCGATATCAAGAGTTCACACGAGGACCAATGCGGATCTACTCTG 600
QY 671 GATGATGTTGTGATGGGCAATTTTACCAAGAGTGCCTGTATPACTTT 730
DB 601 GACGATCGTTGTGATGGGAAATATCTCTCTGCTGCTGTACACGTT 660
QY 731 ATTGCGAGCAGTTTCAATCATACCAATGCTTAAGTTTGGTTCACGTC 790
DB 661 ATTGCTACTAGTTTAAATCATAACTGAGTGTGATCTCAAGAGC 720
QY 791 GTGATGAAGGATACAAATTTGTCAGGATAAAATGTTGTACACATTT 850
DB 721 GTAATGGAAGCTATATTTGTTGTCAGGAAAGAACGTAGTGCAGTGT 780
QY 851 AATTACTGTTACCGCTGTGGGAACATGCGCCCATTAATGGAGATAGATGA 910
DB 781 AACTACTGTTACAGATGTGGAAACATGCGCCCAATTTCTTGAGATTGGAGA 840
QY 911 CGGTCTTTTCTTCAAGTTCGAACACGACCGCGGCAAGTGAACCCAGATG 970
DB 841 CAGAACTTCTTCAATTCGATTCAGACCTAGACAAAGTCGAACCCGATAC 900
QY 971 ACTCTGATTTACTTCTGTAA 991
DB 901 ACCCTGATTTATTTTGTGA 921

RESULT 10
US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3

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; CURRENT APPLICATION NUMBER: US/09/938,842A									
; CURRENT FILING DATE: 2001-08-24									
; PRIOR APPLICATION NUMBER: US 60/227,866									
; PRIOR FILING DATE: 2000-08-24									
; PRIOR APPLICATION NUMBER: US 60/264,647									
; PRIOR FILING DATE: 2001-01-16									
; PRIOR APPLICATION NUMBER: US 60/300,111									
; PRIOR FILING DATE: 2001-06-22									
; NUMBER OF SEQ ID NOS: 5379									
; SEQ ID NO 705									
; LENGTH: 921									
; TYPE: DNA									
; ORGANISM: Arabidopsis thaliana									
; US-09-938-842A-705									
Query Match 41.0%; Score 559.4; DB 3; Length 921;									
Best Local Similarity 75.5%; Pred. No. 2.1e-169; Indels 0; Gaps 0									
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0									
QY	71	ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACGACGTGTGCGAGTGCAGACGCGTTG 130							
DB	1	ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGAGTGTGAAGCCGTTA 60							
QY	131	TCGAGATTGAGGTGAAGACCTATGTGATCAAGCTCGGACGATCTTGCTGGAGAGTGG 190							
DB	61	GGTGAACGACGACGTGAAGATCCTTTGCGATCAAGCTAAAGCGATTCTTGTTCAGGAATAT 120							
QY	191	AAGTCGACGCCGCGAAGTGTCCTGTCACGGTTTGCCTGACATCCATGCCAGTTTCAT 250							
DB	121	AATGTTCAACCGGTTAAGTGTCCGGTTACGGGTATCGGCGGATATCCATGGCCAGTTTAT 180							
QY	251	GATCTCATCGAGCTTTTCCGCATAGGAGGCAAGCGCCGCCACACGAACTACTGTTCATG 310							
DB	181	GACCTAATTGAGCTATTTTGGTATTTGGTGTAAATGCTCTGATACTAATTACTCTTCATG 240							
QY	311	GGCGACTATGFGATCGTGGATATTATTCTGTCGAGACTGTGTGCTCTTAAGTGGCCCTG 370							
DB	241	GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAAAGTCTCTCTATTGGTGGCAATTA 300							
QY	371	AAGTGGGTATAGGGATAGATCACAACTCTTGGGAGGACACGAGACGAGCAGAGT 430							
DB	301	AAGTGGTGTACAGGACAGACTTACGATCTCTGCGAGGGAATCATAGAGCCGTGAGATT 360							
QY	431	ACGCAAGTATATGCTTTCTATGATGAATCCCTGCGGAAAGTATGAAAATGCGAATGTTTGG 490							
DB	361	ACACAGTCTATGTTTTTATGACGAATGCTTTGAGGAATACGGAATGCAATGTGTGG 420							
QY	491	AAGTACTTCACGATCTGTTTCGACTACTGCTCTGACAGTCTCATTTGAGCACAGAGATT 550							
DB	421	AAGTATTTTACGGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGAGTCAAGTT 480							
QY	551	TTTTTGCTTTCATGTTGGTCTGTCTCCATCGTTCGACATTTAGATCACATCGGAGCCCTA 610							
DB	481	TTCTGTTTGATGAGGCGCTTTCACCTTCTCTGATACTCTTGACAAATCTCGAAGCTTG 540							
QY	611	GATCGTATTCAAGAAGTGCSCCAGAGGCGCCGATGTGTGATCTACTCTGGTCTGATCCA 670							
DB	541	GATCGAATACNAGAGTTCCACAGNAGAACAAATGTGCGATCTACTCTGGTCTGATCCC 600							
QY	671	GATGATCGTTGTGATGGGCAATTTCCACAGAGTGCCTGTTTATPACTTTTGGTCAAGAT 730							
DB	601	GACGATCGTTGTGATGGGGAATATCTCCTCGTGGTGTGGTTTACACGCTTTGGACAGGAC 660							
QY	731	ATTGCAGACGATTCAATCATCAACAAATGGTCTAAGTTTGGTTCGACGTCCTCACCAGCTT 790							
DB	661	ATTGCTACTCAGTTTAAATCATAAACAAATGAGCTGAGTCTGATCTCAAGACGCGATCAACTT 720							
QY	791	GTGATGGAAGGATACAAATTGGTGCAGGATAAAAATGTTGTTCACAGTTTTTCACTGCCCCC 850							
DB	721	GTAATGGAAGGCTAATAATTGGTGTTCAGGAAGAAGACGTAGTGCACAGTGTTTAGTGCCACG 780							
QY	851	AATTACTGTTTACCGCTGTGGAAACATGGCCGCCAATAATGGAGATAGATGAACAATGAAT 910							

Db	781	AAC TACTGTTACAGATGTGGAAACATGCCCGCAATTCTTGAGATTGGAGA.		A 840
Qy	911	CGGTCTTTTTTCTTCAGTTTCGAACACGACCCGCGCAAAGTGAACCAGATGT.		G 970
Db	841	CAGAACCTTCCTTCAATTCGATCCAGCACCTTAGACAAGTTCGAACCCGATAC.		G 900
Qy	971	ACTCCTGAATTAATTTCTGTAA 991		
Db	901	ACCCTGATTATTTTGTGA 921		
 RESULT 11 US-10-425-115-149113 ; Sequence 149113, Application US/10425115 ; Publication No. US20040214272A1 ; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K. ; APPLICANT: Zhou, Yihua ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule: ; FILE REFERENCE: 38-21(53222)B ; CURRENT APPLICATION NUMBER: US/10/425,115 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 369326 ; SEQ ID NO 149113 ; LENGTH: 1879 ; TYPE: DNA ; ORGANISM: Zea mays ; FEATURE: ; OTHER INFORMATION: Clone ID: MRT4577_67515C.1 US-10-425-115-149113				
 Query Match 40.8%; Score 556.6; DB 8; Length 18 Best Local Similarity 75.0%; Pred. No. 2.7e-169; Matches 722; Conservative 0; Mismatches 239; Indels 2;				
Qy	37	TTTCGTGCAGGGGGAGGCGAGAGGTTGGGACAATGCCGTCAATGCGAG.	G 96	
Db	158	TTCCTGCGGCGAAGGGAGCGGGCGGACGAGATGCCGTGCGACGGGG.	G 217	
Qy	97	GCAGATAGACAGCTGTGCGAGTCCAAGCCGTTGTCGAGTTGGAGGTGA.	G 156	
Db	218	GCAGATGCGCAGCTGCGCGACTGCAAGTACCTGCCGAGGCGGAGGTCA.	G 277	
Qy	157	TGATCAAGCTCGGACGATCTTGTGTGGAGGAGTGGAACTGCAGCCCGTGA.	T 216	
Db	278	CGACGAGCCCAAGGCCATCTCTTATGGAGAGTGGAACTGCAGCCCCGTGC.	T 337	
Qy	217	CACGGTTTGGGTGACATCCCATGCCAGTTTCATGATCTCATCGAGCTTT.	G 276	
Db	338	CACCGTCTGCGGCGACATCCACGGCCAGTTCTATGACCTCATCGAGCTCT.	G 397	
Qy	277	AGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGCACTATGTGGATC.	A 336	
Db	398	CGGCGACTCTCCGACACCAACTACCTCTTCATGGGCGACTACGTCGATC.	A 457	
Qy	337	TTCTGTGAGACTGTGTGCGTCTTAGTGGCCCTGAGAGTGGGTATAGGG.	C 396	
Db	458	TTCAAGTTGAAAACAGTTTCTCTGTTAGTGGCTTTTGAAGTCCGTTACAGAG.	C 517	
Qy	397	AATCTTGGAGGGAACACGAGAGCAGGACAGATTACGCAAGTATATGGTT.	A 456	
Db	518	AATCTTAGAGAAATCATGAGACGACAAATCACTCAAGTATATGGCT.	A 577	
Qy	457	ATGCGCTCGGAAGTATGGAATTCGGAATGTTTGGAAAGTACTTTCACGGATC.	A 516	
Db	578	ATGCTTAAGAAAAATATGGAATGCAAAATGTCTGGAAGTATTTTACAGACT.	T 637	
Qy	517	CTGCGCTTCGACAGCTCTCATTTAGCAGCAGAGATTTTTTGTCTTCAATGTG.	C 576	
Db	638	TTTGCTCTCAGCTCTTATAGAAAATCAGGCTCTTGTCTTCTCAATGGTG.	C 697	


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; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1761)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118848C.1
US-10-424-599-20866

Query Match      40.1%; Score 547.6; DB 7; Length 1761;
Best Local Similarity 76.5%; Pred. No. 2.1e-165;
Matches 710; Conservative 0; Mismatches 214; Indels 4; Gaps 3;

QY 68 ACAATCGCGTCAATATGCAGATGTAGACGGGAGATAGACGACTGTGGAGTGAAGCGG 127
DB 306 ACGATGCCGTCTCACGCGATCTGAGCGACAGATCGAGCAGCTGATGGACTGCAAGCCT 365

QY 128 TTGTCGGAGTTGGAGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGGAG 187
DB 366 CTGCCGGAGTCGGAGTGAAGCGCTGTGCGATCAAGCGAGGCGGATCTTGTGGAGGAG 425

QY 188 TGGAACTGTCAGCCCGTGAAGTGTCTGTACGGTTTGGCGTGAACATCCATGCCAGTTT 247
DB 426 TGGAACTGTCAGCCCGTGAAGTGTCTGTACGGTTTGGCGTGAACATCCATGCCAGTTT 485

QY 248 CATGATCTCATGAGCTTTCCGATAGGAGCAAGCGGCCCGACAGCACTACTTGTTC 307
DB 486 TAGCATCTCATGAGCTTTCCGATAGGAGCAAGCGCTCCCGATACCAATTTATCTCTTT 545

QY 308 ATGGCGCATGTGTGATCGTGGATATTATCTGTGAGACTGTGT - GCCTCTTATGTGC 366
DB 546 ATGGCGCATGTGTGATCGTGGATATTATCTGTGAGACTGTGT - GCCTCTTATGTGC 605

QY 367 CCTGAAGTGCAGTATAGGATAGGATCAAA - TCTTGGAGGGAACCAAGAGCAGGC 425
DB 606 CTTGAACGTTCTGTTATGAGATAGAAATTAACAATCTTATGGGAAATCATGAAGCCGTC 665

QY 426 AGATTACGCAAGTATATGTTTCTATGATGAATGCTCGGGAAGTATGGAATGGAATG 485
DB 666 AATAAATCAATGATGTTGCTTCTATGATGAATGCTTGGAGAAATATGGAATGCAATG 725

QY 486 TTTGGAAGTACTTACGGATCTGTTGCGACTACTG - CCTCTGACAGCTCTCATTTAGCA 543
DB 726 TCTGGAATACTTACAGACTGTTGATTAATTTGATCTCTGACTGCTGCTTATTTAGAG 785

QY 544 CGAGATTTTTTCTTCTATGTTGTTGTTCTTCTCATGCTCGACACATTAATGACATCG 603
DB 786 TCAGATTTTTTCTTCTATGTTGTTGTTCTTCTCATGCTCGACACATTAATGACATCG 845

QY 604 AGCCCTAGATCGTATTCAGAAAGTCCGCGACGAGGCCCGATGTGTGATCTACTCTGTC 663
DB 846 TGCCCTTGGATCGCATACAGAGGTTTCCACAGAAAGCAATGTGTGACTCTTGTGTC 905

QY 664 TGATCCAGATGATCGTTTGGATGAGGCAATTTCCACAGAGTGGCGTTTACTTTTGG 723
DB 906 TGATCCAGATGATCGTTTGGATGAGGCAATTTCCACAGAGTGGCGTTTACTTTTGG 965

QY 724 TCAAGATATTGACAGCAGTCAATCATACCAATGTTCTTAAGTTTGGTTGACGCTCA 783
DB 966 ACAGGATATAGTGTCTCAGTTTAAATCATACCAATGTTCTCTCCCTGATATCGAGACTCA 1025

QY 784 CCAGCTTGTGATGGAAGGATCAATTTGGTCCAGGATAAATTTGTTCAGATTTTCA 843
DB 1026 CCAGCTTGTGATGGAAGGATCAATTTGGTCCAGGATAAATTTGTTCAGATTTTCA 1085

QY 844 TGCCTCCCAATTAATGTTTACCGCTGTGGGAAATGCGCCGCAATATGAGATGAGTGAAC 903
DB 1086 TGCACCAATTAATGTTTACCGCTGTGGGAAATGCGCCGCAATATGAGATGAGTGAAC 1145

QY 904 AATGAATCGGCTTTTCTTCACTTCAAGTGAACACGACCGCGGCAAGTGAACCAAGTGTGAC 963
DB 1146 TATGATCAGAAATTTTCTGCACTTTGATCCAGTCTCCAGACAAATTTGAGCCCGACACCA 1205
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QY 964 GCGAAGACTCTCGATTACTTTCTGTAA 991
DB 1206 ACGAAGACTCCAGATTATTTTGTAA 1233

RESULT 14
US-09-938-842A-571
; Sequence 571. Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

Query Match      39.0%; Score 531.8; DB 3; Length 92.
Best Local Similarity 73.7%; Pred. No. 1.8e-160;
Matches 677; Conservative 0; Mismatches 242; Indels 0;

QY 73 GCCGTCAATATCCAGATGTAGACCGGAGATAGACAGCTGTCGGAGTGCA 132
DB 6 GCCGCGACCGGAGATATCGATCGTCAGATCGAGCAGCTTATGGAGTGTA 65

QY 133 GGAGTTGGAGTGAAGAACCTATGTATCAAGCTCGGACGATCTTTGGTGG 192
DB 66 TGAAACGGAGTGAAGATGTTGTGTGAGCAGCAAGAGCATCTTGTGG 125

QY 193 CGTGAGCCCGTGAAGTGTCTCTGACAGTTTGGTGGTGAATCCATGGCC 252
DB 126 TCTTCAACCGGTTAAATGTCCGTTACCGTCTGCGGTGATATCCACGGCC 185

QY 253 TCTCATCGAGCTTTTCCGATAGGAGGCAAGCGCCGACACGAACTACT 312
DB 186 TCTAATCGAGCTTTTTCGATCGGTGGTTCTTCTCGATTAATATATC 245

QY 313 CGACTATGTGATCGTGATATTATTTCTGTGAGACTGTGTGCTCTTTAG 372
DB 246 TGATTAATGTGATCGAGGATATTATTTGTGAGACAGTCTCACATTTGG 305

QY 373 GGTGCGGTATAGGATAGGATACAAATCTTGGAGGGAACCAAGAGAGCA 432
DB 306 AGTTCTGTACAGAGATAGACTTACTATCTTAAGAGGAATCATGAAAGCC 365

QY 433 GCAAGTATATGTTTCTATGATGAATGCTCGGAAGTATGGAATGCA 492
DB 366 TCAAGTGTATGGTTTATGATGAATGTTTGGAGGAATATGGAATGCTA 425

QY 493 GTACTTCAAGGATCTGTTTCGACTACCTCCCTCTGACAGCTCTCATTTGAGC 552
DB 426 GCATCTCACTGATCTTTTGTGATTTCTTCCACTTACAGCTCTTATTTGAG 485

QY 553 TGTCTTCAATGGTGTGTCTCCATCGCTCGACATTAATGATACATCC 612
DB 486 CTGTTTACATGGAGACTTTTCACTTCTTTTATAGATACACTTGAACACATCC 545

QY 613 TCGTATTCAAGAAGTGGCCGACGAGGGCCGATGTGTGATCTACTCTGTT 672
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[illegible]

RESULT 15
US-09-938-842A-571
; Sequence 571, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

	Query Match	39.0%	Score 531.8	DB 3	Length 924	
	Best Local Similarity	73.7%	Pred. No. 1.8e-160			
	Matches 677	Conservative 0	Mismatches 242	Indels 0	Gaps 0	
QY	73	GCCTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTCGAGAGTCGAAGCCGTTGTC	132			
Db	6	GCCTGCACCGGAGATATCGATCGTCAGATCGACAGCTTATGAGTGTAAAGCGTTATC	65			
QY	133	GGAGTTGGAGTGAAGAACCTATGTGATCAGCTCGGACGATCTTGGTGAGGAGTCGAA	192			
Db	66	TGAAACGGAGTGAAGATGTTGTGTGACCGCAAGACGATCTTGTGGAAGAGTTAA	125			
QY	193	CGTGACGCCGTGAAGTGTCTGTGTCACGGTTTGGGTGACATCATGGCCAGTTTCATGA	252			
Db	126	TGTTCAACCGGTTAAATGTCCGGTTACCGTGTGGGTGATATCACGGCCAAATTTTACGA	185			
QY	253	TCTCATCGAGCTTTTCCGCATAGAGAGCAAGCGCCCGCAACGAACTACTTGTTCATGGG	312			

Search completed: December 9, 2005, 10:13:43
Job time : 1081 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 07:11:40 ; Search time 242 Seconds
(without alignments)
2108.725 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggaggag.....tatggcagctcgagctgcg 1365

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*
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2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
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9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512.4	37.5	1541	6	US-10-909-125-814
2	46.6	3.4	1864	6	US-10-750-185-37665
3	36.6	2.7	1861	6	US-10-750-185-62270
4	36	2.6	903	7	US-11-074-176-361
5	36	2.6	924	7	US-11-074-176-253
6	34.4	2.5	7292	7	US-11-075-646-5
7	34.2	2.5	2569	6	US-10-750-185-63345
8	34	2.5	175023	7	US-11-121-086-18
9	33.8	2.5	166639	7	US-11-121-086-52
10	33	2.4	491	6	US-10-750-185-3553
11	32.8	2.4	3156	6	US-10-750-185-46888
12	32.8	2.4	124972	7	US-11-121-086-100
13	32.8	2.4	134174	7	US-11-121-086-99
14	32.6	2.4	1614	7	US-11-167-856-21
15	32.6	2.4	1721	6	US-10-750-185-62692
16	32.6	2.4	2480	6	US-10-750-185-25218
17	32.4	2.4	1911	6	US-10-750-185-38730
18	32.2	2.4	949	6	US-10-750-185-55420
19	32.2	2.4	191684	7	US-11-121-086-2
20	32.2	2.4	319608	7	US-11-145-703-1
21	32	2.3	1178	6	US-10-750-185-49333
22	31.8	2.3	600	6	US-10-750-185-835
23	31.8	2.3	875	6	US-10-750-185-44636

C 24	31.8	2.3	2586	6	US-10-750-185-24808	Seq
C 25	31.6	2.3	1118	6	US-10-750-185-61961	Seq
C 26	31.6	2.3	1470	6	US-10-750-185-42558	Seq
27	31.6	2.3	1557	6	US-10-750-185-41027	Seq
28	31.6	2.3	173602	7	US-11-121-086-25	Seq
29	31.4	2.3	828	6	US-10-467-657-2501	Seq
C 30	31.4	2.3	963	6	US-10-467-657-2503	Seq
C 31	31.4	2.3	95223	7	US-11-117-187-211	Seq
C 32	31.4	2.3	1082144	7	US-11-117-187-211	Seq
C 33	31.2	2.3	193789	7	US-11-112-908-55	Seq
C 34	31	2.3	1685	6	US-10-750-185-36877	Seq
C 35	31	2.3	1901	6	US-10-750-185-35821	Seq
C 36	31	2.3	2242	6	US-10-750-185-54495	Seq
37	31	2.3	2730	6	US-10-750-185-52345	Seq
38	31	2.3	126552	7	US-11-121-086-1	Seq
C 39	30.8	2.3	1200	9	US-11-082-389-343	Seq
40	30.8	2.3	2833	7	US-11-110-082-18	Seq
41	30.6	2.2	728	6	US-10-750-185-37667	Seq
42	30.6	2.2	1136	6	US-10-750-185-32673	Seq
C 43	30.6	2.2	189539	7	US-11-121-086-16	Seq
44	30.4	2.2	1149	6	US-10-750-185-42234	Seq
C 45	30.4	2.2	2081	6	US-10-750-185-59335	Seq

ALIGNMENTS

RESULT 1

US-10-909-125-814

; Sequence 814, Application US/10909125

; Publication No. US20050261218A1

; GENERAL INFORMATION:

; APPLICANT: Esau, Christine

; APPLICANT: Lollo, Bridget

; APPLICANT: Bennett, C. Frank

; APPLICANT: Freier, Susan M.

; APPLICANT: Griffey, Richard H.

; APPLICANT: Baker, Brenda F.

; APPLICANT: Vickers, Timothy

; APPLICANT: Marcusson, Eric G.

; APPLICANT: Koller, Eric

; APPLICANT: Swayze, Eric

; APPLICANT: Jain, Ravi

; APPLICANT: Bhat, Balkrishen

; APPLICANT: Peralta, Egen

; TITLE OF INVENTION: Oligomeric Compounds And Compositions For

; FILE REFERENCE: Of Small Non-Coding RNAs

; CURRENT APPLICATION NUMBER: US/10/909,125

; CURRENT FILING DATE: 2004-07-30

; PRIOR APPLICATION NUMBER: US 60/492,056

; PRIOR FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 60/516,303

; PRIOR FILING DATE: 2003-10-31

; PRIOR APPLICATION NUMBER: US 60/531,596

; PRIOR FILING DATE: 2003-12-19

; PRIOR APPLICATION NUMBER: US 60/562,417

; PRIOR FILING DATE: 2004-04-14

; NUMBER OF SEQ ID NOS: 2184

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 814

; LENGTH: 1541

; TYPE: DNA

; ORGANISM: H. sapiens

US-10-909-125-814

Query Match 37.5%; Score 512.4; DB 6; Length 15

Best Local Similarity 71.9%; Pred. No. 4e-161;

Matches 569; Conservative 0; Mismatches 261; Indels 3 0;

QY 86 GATGTAGACCGGACATAGACAGCTGCGAGTGAAGCGGTGTGCGG

DB 46 GAGCTGGACCACTGGTCTGACGCTGAACGAGTGTAGCAGCTGAACG

CG 145

CG 105

146 AAGAACCTATGTATCAAGCTCGGACGATCTTGGTGGAGAGTGGAACGTGACGCCCGTG 205
106 CGGACGCTGTGCGAGAAGCAAGGAAATTTTAAACAAAGAAATCAATGTGTCAAGAGGTT 165
206 AAGTGTCTGTACAGGTTTGGGTCACATCCATGCGCAGTTTCATGATCTCATCGAGCTT 265
166 CGTGGCCCTGTACTGTCTGTGGAGATGTGCATGTGTCAATTTTCATGATCTTTATGGAATC 225
266 TTCCCATAGGAGGCAAGCGCCGACACGAACTACTTGTTCATGGCGCACTATGTGGAT 325
226 TTGAATTTGGTGGAAATCACCGGATACAACTACTTATTTCATGGGTGACTATGTAGAC 285
326 CGTGATATTAATCTGTGAGACTGTGCTGTCTTGTAGTGGCCCTGAAAGTGGGTATAGG 385
286 AGAGGATATTAATCAGTGAGACTGTGACTCTTCTGTAGCATTAAGAGTGGCTTATCCA 345
386 GATAGATCAAGATCTTGGAGGGAACACGAGACGAGGACGATTAACCAAGTATATGGT 445
346 GAAACGATTTACAATATTGAGAGGAATCACGAAAGCCGACAAATTTACCAAGTATATGGC 405
446 TTCTATGATGAATGCTCGGGAAGTATGGAATGGAATGTTTGGAACTACTTTCACGGAT 505
406 TTTTATGATGAATGTCTGGAAGATATGGAAATGCAAGTTCGAAATATTTACAGAT 465
506 CTGTTGACTACCTGCTCTGACAGCTCTCATGTAGACGAGATTTTGTGCTTCATGGT 565
466 CTCCTTGTATTTCTTCCACTTACAGCTTTAGTAGATGGACAGATATCTGCTCCATGGT 525
566 GGTCTGTCTCCATCGCTGACACATTAAGTATCATATCCGAGCCCTAGATCGGTATCAAGAA 625
526 GGCCTCTCTCCATCATAGACACATGGATCATATAAGAGCCCTGGATCGTTTACAGGAA 585
626 GTGCGCACGAGGCGCGATGTGATCTACTCTGCTGTGATCCAGATGATCGTGTGGA 685
586 GTTCCACATAGGCGCCCAATGTGATCTGTATGTCAGATCCAGATGATCGTGTGGA 645
686 TGGGCAATTCACGAGGTCGCGTTATACCTTTTGGTCAAGATATTGACAGAGCAGTTC 745
646 TGGGATTTTCCACGAGTGTGCTGCTACACATTTGGACAAAGACATTTCTGAAACCTTT 705
746 AATCATACAAATGGTCTAAGTTTGGTGTGACGTCTCACCAGCTTGTGATGGAAGATAC 805
706 AACCATGCCAATGGTCTCACACTGTTTCTGTCGCCACACAGCTTGTAAATGGAGGATAC 765
806 AATTGTGTCAGGATAAATGTTGTACAGTTTTCAGTGCCCCCAATTTACTGTTTACCGC 865
766 AATTGTGTCATGTCGGAATGTGTTACCAATTTTCAGTGACCCCAATTTACTGTTATCGT 825
866 TGTGGAAACATGCGCCCAATAATGGAGATAGATGAACAAATGAATCGGTCTTTTCTTCAG 925
826 TGTGGGAACCAAGCTGCTATCATGGAATTTAGATGACACTTTTAAATATTTCTCTTCAA 885
926 TTCGAACAGACGCGCGCAAGTGAACAGATGACGCGGAAGACTCTCGAATTAATTT 985
886 TTTGACCGCGCGCTGCTGCTGAGCCTCATGTTTACACGCGCAGCCACCCAGACTACTTC 945
986 CTGTAACATGCGCTATACATGTTACTTTT 1015
946 CTATAAATTTCTCTGGGAAACCTGCTTTT 975

RESULT 2

US-10-750-185-37665
; Sequence 37665, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37665
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Bovine 19866880394924
US-10-750-185-37665

Query Match 3.4%; Score 46.6; DB 6; Length 196
Best Local Similarity 64.2%; Pred. No. 6.1e-05;
Matches 70; Conservative 0; Mismatches 39; Indels 0;
QY 496 CTTTACGGAATCTGTTCCAGTACCTGCTCTGACAGCTCTCATTTGAGCAGC
DB 1050 CTGCATGGATGCTTTGACTGCTGCTGCCCTGGCTGCCTGATGAACCCAG
QY 556 TCTTCATGGTGTCTGCTCCATCGCTCGACACATTAGATCACATCCGA
DB 1110 GTGTCACGGCGTTTGTTGTTCCAGAGATAAACACTTTTAGATGATATCAGA

RESULT 3

US-10-750-185-62270
; Sequence 62270, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62270
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Bovine 19866880123096
US-10-750-185-62270

Query Match 2.7%; Score 36.6; DB 6; Length 186
Best Local Similarity 65.1%; Pred. No. 0.13;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
QY 229 TGACATCCATGGCCAGTTTTCATGATCTCATCGAGCTTTTCGCGCATAGGAG
DB 1620 TGCCCTTCTTTATAGTTTATGACCTTTTGTGAAGTGTTCAGAACTGGAG
QY 289 CGACACGAACACTTGTTCATGG 311
DB 1680 TGACACAACTACATATTTATGG 1702

RESULT 4

US-11-074-176-361
; Sequence 361, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.

```

; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(903)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1201; GTP-binding protein Era
US-11-074-176-361

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Query Match          2.6%; Score 36; DB 7; Length 903;
Best Local Similarity 48.1%; Pred. No. 0.13;
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 887 ATGGAGATAGATGAACAAATGAATCGGTCCTTTCTTCAGTTCGAACCCAGCACCGGCGCAA 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 ATTGGTATTGATGATTGCTCAATCAATCTATAAGTATTTACCAGCAGGACCACAATAT 531

QY 947 AGTGAACAGATGTCACGGGAGACTCTCTGATTAATCTTCTGTAACATGGCCTATACAT 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 TATGATGAGATCAGATCAGATCAGATCGTCTCTGAATATTTTGGTTGCGAAGCTTATTCGA 591

QY 1007 GGTACCTTTTACTTACTGAATTTCTGTATAGTACACCTTCATCGAAGCAGTTTGGCCCC 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 GAACAAATTTTACGACTTACTTCTCAAGAAAGTTCACATGCTACTGCGAGTTGTAGTCGAT 651

QY 1067 TGAATGAAGATACCTCCCTCATGATCTAGTAGT 1098
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Db 652 CAAATGAATAAGCATCAAAATGGTAAATTAGT 683

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RESULT 5
US-11-074-176-253
; Sequence 253, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(924)

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1201; GTP-binding protein Era
US-11-074-176-253

Query Match          2.6%; Score 36; DB 7; Length 924;
Best Local Similarity 48.1%; Pred. No. 0.13;
Matches 102; Conservative 0; Mismatches 110; Indels 0;

QY 887 ATGGAGATAGATGAACAAATGAATCGGTCCTTTCTTCAGTTCGAACCCAGC 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 ATTGGTATTGATGATTGCTCAATCAATCTATAAGTATTTACCAGCAGC 552

QY 947 AGTGAACAGATGTCACGGGAGACTCTCTGATTAATCTTCTGTAACATG 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 TATGATGAGATCAGATCAGATCAGATCGTCTCTGAATATTTTGGTTGCGAG 612

QY 1007 GGTACCTTTTACTTACTGAATTTCTGTATAGTACACCTTCATCGAAGC 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 GAACAAATTTTACGACTTACTTCTCAAGAAAGTTCACATGCTACTGCGAGT 672

QY 1067 TGAATGAAGATACCTCCCTCATGATCTAGTAGT 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 673 CAAATGAATAAGCATCAAAATGGTAAATTAGT 704

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RESULT 6
US-11-075-646-5/c
; Sequence 5, Application US/11075646
; Publication No. US20050261223A1
; GENERAL INFORMATION:
; APPLICANT: Czech, Michael P.
; APPLICANT: Powelka, Aimee
; APPLICANT: Guilherme, Adilson L.
; APPLICANT: Cherniack, Andrew D.
; TITLE OF INVENTION: RI140 REGULATION OF DIABETES
; FILE REFERENCE: 17738-009001
; CURRENT APPLICATION NUMBER: US/11/075,646
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,677
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-075-646-5

```

```

Query Match          2.5%; Score 34.4; DB 7; Length 729
Best Local Similarity 53.8%; Pred. No. 1.8;
Matches 71; Conservative 0; Mismatches 61; Indels 0;

QY 137 TTGGAGGTGAAGAACCCTATGTGATCAAGCTCGGACGATCTTTGGTGGAGG 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3064 TTAAATTCAGATCAATTTCTGCTAAATTTTCAGCTCTTCTCTGGTTAAGC 3005

QY 197 CAGCCCGTGAAGTGTCTGTCAACGGTTTTCGGGTGACATCCATGGCCAGT 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3004 CAGTACTTCTGGGCACTGTGATTTGTTGACGATCAACAATGTTGTTT 2945

QY 257 ATCGAGCTTTTC 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2944 AAATGGATTTC 2933

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RESULT 7
US-10-750-185-63345
; Sequence 63345, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

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```
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63345
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: Bovine 19866880467000
US-10-750-185-63345

Query Match      2.5%; Score 34.2; DB 6; Length 2569;
Best Local Similarity 64.6%; Pred. No. 1.1;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1087 TCATCTAGTAGTATGAAGTATCTCTTTGAAGTGTGTGTTCCCTTTTGTAGTACTTCT 1146
DB 1745 TTATATATTGGTAAAGTAAATAAATCAAAATGTTGCTACTAATTAATGATGTACATACT 1804

QY 1147 CCTCTGTTTCATTCATAAAG 1165
DB 1805 ACTGTGTTCTTCATANAG 1823

RESULT 8
US-11-121-086-18
; Sequence 18, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 175023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-18

Query Match      2.5%; Score 34; DB 7; Length 175023;
Best Local Similarity 43.9%; Pred. No. 22;
Matches 145; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 901 AACAAATGAATCGTCTTTTCTTCAGTTCGAACACGACCGCGGCAAGTGAACACCATGT 960
DB 99987 AACTCCCAATGTCCTCTCCCTCAGCCCGGCAACCAACCATTCATATTTCTGTCTGTAT 100046

QY 961 GACGGGGAAGATCCCTGATTACTTTCTGTAACATGGCCCTATACATGGTACCTTTTACTT 1020
DB 100047 GAATTGACTATTCAGGTAATTCATATAAGTGAATCATACAGTATTTGCTTTTGTG 100106

QY 1021 ACTGAATGTTCTGTATAGTACCTTCCATGAGCAGTTTCCCTCCCTGAATGAATACT 1080
DB 100107 ACTGGCTTATTCATTAGACATAATGTCCTCAAGGCTCATCGGTGTGTAATGATGTCA 100166

QY 1081 CCTCATGATCTAGTAGTATGAAGTTATCTCTTTGAAGTGTGTTGTCCTTTTGTAGTA 1140
DB 100167 GAATTTTCTCTTTTAAAGGATAATATTTTCATTCAAATGATATAGACCACATTTTGT 100226
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QY 1141 CTTGCTCTCTGTTTCATTATAAAGTTGCGCTTCAGAACAACTGAGATGTTT
DB 100227 ATCATTTCATCTGTTGATGAGCACTTAGGCTGCTTCTAGCTCTTGCGCTATT
QY 1201 CTGCGACAAGAGGAGCAGTGTCAATGGTTG 1230
DB 100287 TTGCTATGAACATGGGTGTACCAATATTTG 100316

RESULT 9
US-11-121-086-52
; Sequence 52, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 166639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-52

Query Match      2.5%; Score 33.8; DB 7; Length 166
Best Local Similarity 58.4%; Pred. No. 25;
Matches 59; Conservative 0; Mismatches 42; Indels 0;

QY 805 CAATTGGTGCCAGGATAAATAATGTTGTACAGTGTTCAGTGCCTCCCAATT.
DB 116286 CAATTGGGCTAGGATCAGCAGGATGGTTCTTCTGTTATTGCTCGGAATC.

QY 865 CTGTGGGAACATGCGCGCCATAATGAGATAGATGAACAA 905
DB 116346 CTGCAGATATTGTCATCTGTAGTGGGCTGAATAATCTAA 116386

RESULT 10
US-10-750-185-3553/c
; Sequence 3553, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3553
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Bovine MMBT13351
US-10-750-185-3553

Query Match      2.4%; Score 33; DB 6; Length 491;
Best Local Similarity 54.5%; Pred. No. 0.86;
Matches 91; Conservative 0; Mismatches 70; Indels 1;
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RESULT 12
US-11-121-086-100
; Sequence 100, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100

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RESULT 14
US-11-167-856-21/c
; Sequence 21, Application US/11167856
; Publication No. US2005028352A1
; GENERAL INFORMATION:
; APPLICANT: Nikoglav, Basil J
; APPLICANT: Wurtele, Eve S
; APPLICANT: Oliver, David J
; APPLICANT: Behal, Robert
; APPLICANT: Schnable, Patrick S
; APPLICANT: Ke, Jinshan
; APPLICANT: Johnson, Jerry L
; APPLICANT: Allred, Carolyn C
; APPLICANT: Facland, Beth
; APPLICANT: Lutziger, Isabelle
; APPLICANT: Wen, Tsui-Jung
; TITLE OF INVENTION: Materials and Methods for
; TITLE OF INVENTION: Acetyl CoA Levels
; FILE REFERENCE: P2194USDIV-2
; CURRENT APPLICATION NUMBER: US/11/1-13
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/293
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/344
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/090
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ IDS NOS: 38
; SOFTWARE Patent In Ver. 3.1

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; SEQ ID NO 21
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
US-11-167-856-21

Query Match      2.4%; Score 32.6; DB 7; Length 1614;
Best Local Similarity 49.1%; Pred. No. 2.6;
Matches 86; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 753 CCAATGGTCTAAGTTTGGTTGCACGTGTCACACAGCTTGATGGAAGATACAAATTGGT 812
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1237 CCAAGATTTCATCTTGGTATATCTTCATATCTCAGTGACATCTGCCAATATAGTTGGT 1178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 813 GCCAGATAAAATGTGTACAGTCTTTCAGTGCCCCCAATTTACTGTTACCGCTGTGGGA 872
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1177 TGGATGAATATCCCTTGTCTCCAATGGCTTTTCTCCAGTTTAATAAGTGGCTCCTTCG 1118
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 873 ACATGCCGCCCAATATGGAGATAGATGAACAATGAATCGGTCTTTTCTTCAGTT 927
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1117 TTTTACCGTGTCTCAATGTAGATAGAATCTTCTCAAACTGTCTTTTATCCACTT 1063
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-750-185-62692
; Sequence 62692, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 62692
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Bovine 19866880961460
US-10-750-185-62692

Query Match      2.4%; Score 32.6; DB 6; Length 1721;
Best Local Similarity 50.3%; Pred. No. 2.8;
Matches 80; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 975 CTGATTACTTTCTGTAAACATGCGCTATACATGGTACCTTTTACTTACTGAATTCGTCG 1034
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1420 CTGAAAGTCAGTGAATAACAATGATATCAGGTATTCATATACTCTCTGATTATA 1479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1035 TATAGTCACCTTCCCATGGAAGCAGTTTGCCCTGAAATGAAGATACTCCCTCATGATCTAG 1094
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1480 TTCACCTTTGGATCAATGTAGGACAGTTGTCTAAGAATAAATAAATAGGTGATGTTAG 1539
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1095 TAGTATGAAGTTATCTTCTTTGAAAGTGTGTTGCCCTTT 1133
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1540 AAGACTGAATTTGACTAGTCTTTAGCTCTTTTATCCCTTTT 1578
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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CC transport of one or more compounds and modulation of stress resistance.
CC The gene is also useful for identifying and/or cloning PHSRP homologues
CC in other cell types and organisms, for identifying an organism as being
CC P. patens or its close relative and for evolutionary and protein
CC structural studies. The present sequence is that of a PHSRP of the
CC invention
XX
XX Sequence 306 AA;
SQ
Query Match 100.0%; Score 1670; DB 5; Length 306;
Best Local Similarity 100.0%; Pred. No. 7.7e-165;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSVADVDRIEQLESECKPLSEVKNLDCQARTILVEENWVQPKVPTVCGDIHGQFH 60
DB 1 MPSVADVDRIEQLESECKPLSEVKNLDCQARTILVEENWVQPKVPTVCGDIHGQFH 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVVKVYRDRTITILRGHESRQI 120
DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVVKVYRDRTITILRGHESRQI 120
QY 121 TQVYGFYDECLRKYGNNVWKYFTDLYPLTALIEHEIFCLHGLSPSLDTHIRAL 180
DB 121 TQVYGFYDECLRKYGNNVWKYFTDLYPLTALIEHEIFCLHGLSPSLDTHIRAL 180
QY 181 DRIQVPHGPMCDLLWSDDPDRCGWGISPRGAGYTFGQDIAEQNFHTNGLSVARAHL 240
DB 181 DRIQVPHGPMCDLLWSDDPDRCGWGISPRGAGYTFGQDIAEQNFHTNGLSVARAHL 240
QY 241 VMEGYNWCQDKNVVTFVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
DB 241 VMEGYNWCQDKNVVTFVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 2
ABG74203
ID ABG74203 standard; protein; 306 AA.
AC ABG74203;
XX
XX 08-APR-2003 (first entry)
XX
XX P. patens protein phosphatase PP2A-4.
XX
XX Plant; enzyme; PP2A-4; protein phosphatase; PHSRP; cold; transgenic;
KW phosphatase stress related protein; environmental stress; drought;
KW salt tolerance.
XX
XX Physcomitrella patens.
XX
XX US2002152502-A1.
XX
XX 17-OCT-2002.
XX
XX 06-APR-2001; 2001US-00828302.
XX
XX 07-APR-2000; 2000US-0196001P.
XX
XX (SILV/) DA COSTA E SILVA O.
PA (BOHN/) BOHNERT H J.
PA (VTHI/) VAN THIELEN N.
PA (CHEN/) CHEN R.
PA (ISHI/) ISHITANI M.
XX
XX Da Costa E SilvaO, Bohnert HJ, Van Thielen N, Chen R, Ishitani M;
PI
XX WPI; 2003-198392/19.
DR N-PSDB; ABX16239.
XX

PT New transgenic plant cell transformed by a Phosphatase Stre:
PT Protein (PHSRP) coding nucleic acid, useful for modifying s
XX tolerance of a plant.
XX Claim 16; Fig 3C; 79pp; English.
XX
XX The invention relates to a transgenic plant cell transforme
CC Phosphatase Stress-Related Protein (PHSRP) coding nucleic a
CC expression of the nucleic acid in the plant cell results in
CC tolerance to an environmental stress (e.g. salt tolerance, d
CC drought) as compared to a wild type variety of the plant ce
CC include a transgenic plant comprising the novel plant c
CC produced by the transgenic plant of (where the seed is true
CC an increased tolerance to environmental stress as compared
CC variety of the plant cell, an agricultural product produce
CC or seed, an isolated PHSRP or PHSRP coding nucleic acid, a
CC expression vector comprising the nucleic acid, and produc
CC plant containing PHSRP nucleic acid. The transgenic plant c
CC transformed by a Phosphatase Stress-Related Protein (PHSRP)
CC nucleic acid is useful for modifying stress tolerance of a
CC present sequence represents the PHSRP, protein phosphatase,
XX
XX Sequence 306 AA;
SQ
Query Match 100.0%; Score 1670; DB 6; Length 30
Best Local Similarity 100.0%; Pred. No. 7.7e-165;
Matches 306; Conservative 0; Mismatches 0; Indels
QY 1 MPSVADVDRIEQLESECKPLSEVKNLDCQARTILVEENWVQPKVPTV 60
DB 1 MPSVADVDRIEQLESECKPLSEVKNLDCQARTILVEENWVQPKVPTV 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVVKVYRDRTIT 120
DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVVKVYRDRTIT 120
QY 121 TQVYGFYDECLRKYGNNVWKYFTDLYPLTALIEHEIFCLHGLSPS 180
DB 121 TQVYGFYDECLRKYGNNVWKYFTDLYPLTALIEHEIFCLHGLSPS 180
QY 181 DRIQVPHGPMCDLLWSDDPDRCGWGISPRGAGYTFGQDIAEQNFHTNG 240
DB 181 DRIQVPHGPMCDLLWSDDPDRCGWGISPRGAGYTFGQDIAEQNFHTNG 240
QY 241 VMEGYNWCQDKNVVTFVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAP 300
DB 241 VMEGYNWCQDKNVVTFVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAP 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 3
ABP98034
ID ABP98034 standard; protein; 306 AA.
XX
XX AC ABP98034;
XX
XX 11-AUG-2003 (first entry)
XX
XX Protein phosphatase stress-related polypeptide GmPP2A-5.
DE
XX Protein phosphatase stress-related polypeptide; PHSRP; PpPP
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
KW drought; salinity; cold; enzyme.
XX
XX Glycine max.
XX
XX WO2003020914-A2.
XX
XX 13-MAR-2003.
PD

XX 05-SEP-2002; 2002WO-US028445.
XX 05-SEP-2001; 2001US-0317305P.
XX (BADI) BASF PLANT SCI GMBH.
XX Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa E Silva O;
XX WPI; 2003-300886/29.
XX N-PSDB; ACC43349.
XX New protein phosphatase stress-related polypeptide coding nucleic acid,
XX useful for modulating plant's tolerance to an environmental stress such
XX as drought, increased salinity and cold.
XX Claim 14; Page 82-83; 107pp; English.
XX The present sequence represents a protein phosphatase stress-related
XX polypeptide (PPSRP). The specification describes PPSRP polypeptides
XX designated Pp2A-1, Pp2A-2, BnPP2A-1, BnPP2A-2, GmPP2A-1,
XX GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from
XX Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
XX polypeptides and polynucleotides are useful for modulating plant
XX tolerance to an environmental stress such as drought or increased
XX salinity and cold. They are also useful in identification and
XX localization of Physcomitrella patens, Brassica napus, Glycine max or
XX Oryza sativa and related organisms, mapping of genomes of organisms
XX related to the above species, in a evolutionary and polypeptide
XX structural studies, in determination of PPSRP regions required for
XX function, modulation of PPSRP activity, modulation of metabolism of one
XX or more cell functions and transmembrane transport of one or more
XX components
XX Sequence 306 AA;
Query Match 92.8%; Score 1549; DB 6; Length 306;
Best Local Similarity 91.5%; Pred. No. 3.1e-152;
Matches 280; Conservative 16; Mismatches 10; Indels 0; Gaps 0;
QY 1 MPSADVDRQIEQLSECKPLSEVKNLCOARTILVEENWVQPKCVTVCGDIHQGFH 60
DB 1 MPSHADLERQIEQLMDCKPLSEVKALCOARTILVEENWVQPKCVTVCGDIHQGFY 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILRGHESRQI 120
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILRGHESRQI 120
QY 121 TQVGYFYDECLRKYGNNVWKYFTDLFDLPLTALIEHIEIFCLHGLSPSLDTHIRAL 180
DB 121 TQVGYFYDECLRKYGNNVWKYFTDLFDLPLTALIEHIEIFCLHGLSPSLDTHIRAL 180
QY 181 DRIQVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFQODIAEQNHTNGSLVARAHL 240
DB 181 DRIQVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFQODIAEQNHTNGSLVARAHL 240
QY 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
DB 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 4
ID ABP98039
XX ABP98039 standard; protein; 306 AA.
XX AC ABP98039;
XX 11-AUG-2003 (first entry)
XX

DE Protein phosphatase stress-related polypeptide OsPP2A-5.
XX Protein phosphatase stress-related polypeptide; PPSRP; Pp2A-1;
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
KW drought; salinity; cold; enzyme.
XX Oryza sativa.
XX WO2003020914-A2.
XX 13-MAR-2003.
XX 05-SEP-2002; 2002WO-US028445.
XX 05-SEP-2001; 2001US-0317305P.
XX (BADI) BASF PLANT SCI GMBH.
XX Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa E;
XX WPI; 2003-300886/29.
XX N-PSDB; ACC43354.
XX New protein phosphatase stress-related polypeptide coding r
XX useful for modulating plant's tolerance to an environmental
XX as drought, increased salinity and cold.
XX Claim 18; Page 88; 107pp; English.
XX The present sequence represents a protein phosphatase stress
XX polypeptide (PPSRP). The specification describes PPSRP poly
XX designated Pp2A-1, Pp2A-2, BnPP2A-1, BnPP2A-2, BnPP2A-3,
XX GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
XX Physcomitrella patens, Brassica napus, Glycine max or Oryza
XX polypeptides and polynucleotides are useful for modulating
XX tolerance to an environmental stress such as drought or inc
XX salinity and cold. They are also useful in identification a
XX localization of Physcomitrella patens, Brassica napus, Glyc
XX Oryza sativa and related organisms, mapping of genomes of c
XX related to the above species, in a evolutionary and polypep
XX structural studies, in determination of PPSRP regions requi
XX function, modulation of PPSRP activity, modulation of metat
XX or more cell functions and transmembrane transport of one c
XX components
XX Sequence 306 AA;
Query Match 92.6%; Score 1547; DB 6; Length 306
Best Local Similarity 91.5%; Pred. No. 5e-152;
Matches 280; Conservative 15; Mismatches 11; Indels
QY 1 MPSADVDRQIEQLSECKPLSEVKNLCOARTILVEENWVQPKCVTV 60
DB 1 MPSHADLERQIEQLMECKPLSEVKALCOARTILVEENWVQPKCVTV 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITI 120
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITI 120
QY 121 TQVGYFYDECLRKYGNNVWKYFTDLFDLPLTALIEHIEIFCLHGLSPSE 180
DB 121 TQVGYFYDECLRKYGNNVWKYFTDLFDLPLTALIEHIEIFCLHGLSPSE 180
QY 181 DRIQVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFQODIAEQNHTNG 240
DB 181 DRIQVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFQODIAEQNHTNG 240
QY 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAE 300
DB 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAE 300
QY 301 TPDYFL 306

Db	301 TPDVFL 306		PR	18-JUN-1999;	99US-0139455P.
			PR	18-JUN-1999;	99US-0139456P.
			PR	18-JUN-1999;	99US-0139457P.
			PR	18-JUN-1999;	99US-0139458P.
			PR	18-JUN-1999;	99US-0139459P.
			PR	18-JUN-1999;	99US-0139460P.
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 37969.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0121800P.

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Best Local Similarity 90.7%; Score 1514; DB 3; Length 306;

Matches 273; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

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Qy	181	DRIQVPHGPMCDLIWSDPDDRCWGIISPRCAGYTFQODIATQFNHNGLSISRAHQL	240
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Qy	241	VMEGYNWQDKNNVTVFAPNYCYRCGNMAAIMEIDETWNRSLFQEPAPROSEPDVTRK	300
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RESULT 9
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ID AAG40766 standard; protein; 306 AA.
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DT	18-OCT-2000	(first entry)
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KW	Protein identification;	signal transduction pathway; metabo-
KW	hybridisation assay;	genetic mapping; gene expression contr-
KW	termination sequence;	corn.
XX		
OS	Zea mays	subsp. mays.
XX		
FN	EPI033405-A2.	
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PD	06-SEP-2000.	
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PF	25-FEB-2000;	2000EP-00301439.
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Matches 272; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
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Db 301 TPDYFL 306

RESULT 12
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ID AAG36033 standard; protein; 306 AA.
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AC AAG36033;
XX
DT 18-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 44102.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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OS Zea mays subsp. mays.
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QY 241 VMEGYNMCDKNVTVTFSAFNPCYRCGNMAAIMEIDETMNRSLQFEPAF
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DB 301 TPDYFL 306

RESULT 13
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AC AAG29592;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabo
KW hybridisation assay; genetic mapping; gene expression contr
KW termination sequence.
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OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
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PR 19-JUL-1999; 99US-0144333P.
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PR 20-JUL-1999; 99US-0144632P.
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PR 21-JUL-1999; 99US-0144814P.
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PR 21-JUL-1999; 99US-0145088P.
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PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
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PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
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PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151067P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.

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PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
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PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 89.5%; Score 1495; DB 3; Length 307;
Best Local Similarity 87.9%; Pred. No. 1.3e-146;
Matches 268; Conservative 23; Mismatches 14; Indels 0; Gaps 0;

QY 2 PSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEYNQPVKCVTVCGDIHGQFHD 61
DB 3 FATGDIHQIEQLMECKALSETEVKMLCEHAKTILVEEYNQPVKCVTVCGDIHGQFYD 62
QY 62 LIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLLVALKVRYDRITILRGNHESRQIT 121
DB 63 LIELFRIGGSPDNTNLFMGDYVDRGYYSVETVSLLVALKVRYDRITILRGNHESRQIT 122
QY 122 QVGYFDCLRKYGNNVWKVPTDLDYLPPLTALIEHIFCLHGLSPSLDTLDIRALD 181
DB 123 QVGYFDCLRKYGNNVWKVPTDLDYLPPLTALIEHIFCLHGLSPSLDTLDIRALD 182
QY 182 RQIEVPHGPMCDLLWSPDDRCGWIISPRGAGYTFGQDIATQFNHTNGLSLISRAHQLV 241
DB 183 RQIEVPHGPMCDLLWSPDDRCGWIISPRGAGYTFGQDIATQFNHTNGLSLISRAHQLV 242
QY 242 MEGFNWQCKNVTVVFSAPNYCYRCGNMAAIMEIDTNMRSFLOPEAPROSEPQVTRKT 301
DB 243 MEGFNWQCKNVTVVFSAPNYCYRCGNMAAIMEIDTNMRSFLOPEAPROSEPQVTRKT 302
QY 302 PDYFL 306
DB 303 PDYFL 307

RESULT 14
ADT56656
ID ADT56656 standard; protein; 304 AA.
XX AC ADT56656;
XX DT 13-JAN-2005 (first entry)
XX DE Plant polypeptide, SEQ ID 6733.
XX KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
```

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XX Viridiplantae.
OS US2004216190-A1.
PN 28-OCT-2004.
PD 18-DEC-2003; 2003US-00739930.
PF 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX (KOVA/) KOVALIC D K.
PI Kovalic DK;
DR WPI; 2004-757369/74.
XX New recombinant DNA constructs useful in the field of bioch
PT Genetics, and in particular for producing transgenic plants
PT biological characteristics.
XX Claim 2; SEQ ID NO 6733; 14pp; English.
CC The invention relates a recombinant DNA construct compris
CC polynucleotide having any of 5544 nucleotide sequences (cDN
CC 1-5544) and encoding a polypeptide with any of 5544 amino a
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from cc
CC Arabidopsis, wheat and rape but the specification does not
CC sequences is derived from which organism. Also included is
CC producing a plant having an improved property, comprising t
CC plant with a recombinant DNA construct comprising a promote
CC functional in a plant cell operably joined to a polynucleot
CC polypeptide associated with the property, and growing the t
CC plant. The property is selected from improving plant cold t
CC manipulating growth rate in plant cells by modification of
CC pathway, for improving plant drought tolerance, for providi
CC resistance to plant disease, for galactomannan production,
CC of plant growth regulators, for improving plant heat tolera
CC improving plant tolerance to herbicides, for increasing the
CC homologous recombination in plants, for lignin production,
CC plant tolerance to extreme osmotic conditions, for improvin
CC tolerance to pathogens or pests, for yield improvement by n
CC photosynthesis, for modifying seed oil yield and/or content
CC modifying seed protein yield and/or content, for yield impr
CC modification of carbohydrate, nitrogen or phosphorus use ar
CC and for yield improvement by providing improved plant grow
CC development under at least one stress condition. The polyn
CC also encode a plant transcription factor. The methods and c
CC the present invention are useful in the field of biochemist
CC biological characteristics such as increased yield, improve
CC flow, increasing plant tolerance to cold or heat, improving
CC tolerance to extreme osmotic and drought conditions, and in
CC tolerance to plant pests or pathogens. They can also be use
CC arrays of molecules, plant breeding markers, computer-based
CC analysis systems. The present sequence is one of the 5544 f
CC sequences of the invention. Note: The sequence data for thi
CC not form part of the printed specification, but was obtaine
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.
XX Sequence 304 AA;
SQ
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Query Match 89.0%; Score 1486; DB 8; Length 304
Best Local Similarity 88.2%; Pred. No. 1.1e-145;
Matches 270; Conservative 16; Mismatches 18; Indels
QY 1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEYNQPVKCPVT
DB 1 MPSNGDLDRQIEQLMECKALSEADVKILCDQAKAILVEEYNQPVKCPVI
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLLVALKVRYDRITTI
s 1;
FH 60
FY 60
QI 120
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PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 05-AUG-1999; 99US-0147302P.
 PR 06-AUG-1999; 99US-0147192P.
 PR 07-AUG-1999; 99US-0147260P.
 PR 08-AUG-1999; 99US-0147303P.
 PR 09-AUG-1999; 99US-0147416P.
 PR 10-AUG-1999; 99US-0147493P.
 PR 11-AUG-1999; 99US-0148171P.
 PR 12-AUG-1999; 99US-0148319P.
 PR 13-AUG-1999; 99US-0148341P.
 PR 14-AUG-1999; 99US-0148565P.
 PR 15-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149168P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149428P.
 PR 19-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 21-AUG-1999; 99US-0149902P.
 PR 22-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 24-AUG-1999; 99US-0150568P.
 PR 25-AUG-1999; 99US-0150884P.
 PR 26-AUG-1999; 99US-0151065P.
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 PR 30-AUG-1999; 99US-0151438P.
 PR 31-AUG-1999; 99US-0151930P.
 PR 01-SEP-1999; 99US-0152363P.
 PR 02-SEP-1999; 99US-0153070P.
 PR 03-SEP-1999; 99US-0153758P.
 PR 04-SEP-1999; 99US-0154018P.
 PR 05-SEP-1999; 99US-0154033P.
 PR 06-SEP-1999; 99US-0154779P.
 PR 07-SEP-1999; 99US-0155139P.
 PR 08-SEP-1999; 99US-0155486P.
 PR 09-SEP-1999; 99US-0155659P.
 PR 10-SEP-1999; 99US-0156458P.
 PR 11-SEP-1999; 99US-0156596P.
 PR 12-SEP-1999; 99US-0157117P.
 PR 13-SEP-1999; 99US-0157533P.
 PR 14-SEP-1999; 99US-0157865P.
 PR 15-SEP-1999; 99US-0158029P.
 PR 16-SEP-1999; 99US-0158232P.
 PR 17-SEP-1999; 99US-0158369P.
 PR 18-SEP-1999; 99US-0159293P.
 PR 19-SEP-1999; 99US-0159294P.
 PR 20-SEP-1999; 99US-0159295P.
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 PR 22-SEP-1999; 99US-0159330P.
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 PR 25-SEP-1999; 99US-0159638P.
 PR 26-SEP-1999; 99US-0159584P.
 PR 27-SEP-1999; 99US-0160741P.
 PR 28-SEP-1999; 99US-0160767P.
 PR 29-SEP-1999; 99US-0160768P.
 PR 30-SEP-1999; 99US-0160770P.
 PR 01-OCT-1999; 99US-0160814P.
 PR 02-OCT-1999; 99US-0160815P.
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 PR 04-OCT-1999; 99US-0160980P.
 PR 05-OCT-1999; 99US-0160981P.
 PR 06-OCT-1999; 99US-0160989P.
 PR 07-OCT-1999; 99US-0161404P.
 PR 08-OCT-1999; 99US-0161405P.
 PR 09-OCT-1999; 99US-0161406P.
 PR 10-OCT-1999; 99US-0161359P.
 PR 11-OCT-1999; 99US-0161360P.
 PR 12-OCT-1999; 99US-0161361P.
 PR 13-OCT-1999; 99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.
 PR 29-OCT-1999; 99US-0161993P.
 PR 30-OCT-1999; 99US-0162142P.
 Query Match 87.9%; Score 1468; DB 3; Length 292
 Best Local Similarity 90.4%; Pred. No. 7.9e-144;
 Matches 263; Conservative 16; Mismatches 12; Indels

QY 16 ECKPLSELEVKNLCDQARTILVEEWNVQPKCPVTVCGDHGHDLIEL
 DB 2 ECKPLSEADVRFLCDQARAILVEEYNVQPKCPVTVCGDHGHQFYDLIEL
 QY 76 NYLFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGHNHESRQITQVYC
 DB 62 NYLFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGHNHESRQITQVYC
 QY 136 NANVWKYFTDLFDYLPALTALIEHEIFCLHGGGLSPSLDTHIRALDRIOE
 DB 122 NANVWKYFTDLFDYLPALTALIESQVFCFLHGGGLSPSLDTHIRALDRIOE
 QY 196 LWSDDDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQIWMSEY
 DB 182 LWSDDDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQIWMSEY
 QY 256 VFSAPNYCYRCGNMAAIMEIDETWNRSLQFEPAPRQSEPDVTRKTPDYF
 DB 242 VFSAPNYCYRCGNMAAILEIGENMEQNFLODPAPRQVEPDTRKTPDYF

Search completed: December 9, 2005, 10:20:24
 Job time : 139 secs

s 0;
 DT 75
 DT 61
 YG 135
 YG 121
 DL 195
 DL 181
 VT 255
 VT 241

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Result No.	Score	Query Match	Length	DB ID	Description
1	1522	91.1	306	2	S31162 phosphoprotein pho
2	1508	90.3	306	2	S31161 phosphoprotein pho
3	1501.5	89.9	305	2	S37086 phosphoprotein pho
4	1495	89.5	307	1	B96722 phosphoprotein pho
5	1481	88.7	306	2	T03389 probable phosphopro
6	1445	86.5	302	2	T03559 phosphoprotein pho
7	1427	85.4	309	1	A27430 phosphoprotein pho
8	1427	85.4	309	1	PAHU2A phosphoprotein pho
9	1427	85.4	309	1	PAB8A1 phosphoprotein pho
10	1427	85.4	309	1	PART2A phosphoprotein pho
11	1427	85.4	309	1	S10371 phosphoprotein pho
12	1421	85.1	309	1	S20348 phosphoprotein pho
13	1412	84.6	309	1	S12961 phosphoprotein pho
14	1411	84.5	309	1	PAHU2B phosphoprotein pho
15	1411	84.5	309	1	PART2B phosphoprotein pho
16	1411	84.5	309	1	PART2B phosphoprotein pho
17	1410	84.4	309	1	JC4316 phosphoprotein pho
18	1388	83.1	318	1	T21975 phosphoprotein pho
19	1386	83.0	313	1	S52860 phosphoprotein pho
20	1385	82.9	308	2	S31163 phosphoprotein pho
21	1385	82.9	313	1	S52659 phosphoprotein pho
22	1377	82.5	293	2	B27430 phosphoprotein pho
23	1375	82.3	313	1	S35502 phosphoprotein pho
24	1367	81.9	322	2	B36076 phosphoprotein pho
25	1360.5	81.5	314	2	T09996 phosphoprotein pho
26	1358	81.3	309	2	S12986 phosphoprotein pho
27	1346	80.6	314	2	T03660 phosphoprotein pho
28	1328	79.5	309	2	A36076 phosphoprotein pho
29	1328	79.5	325	2	A8029 phosphoprotein pho

Db 63 LIELFRIGGSPDNYLFMGDYVDRGYYSVETVSLVALLVKKVYRDLTILRGNHESRQIT 122
QY 122 QVGYFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRALD 181
Db 123 QVGYFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRALD 182
QY 182 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLV 241
Db 183 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLV 242
QY 242 MEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETWNRSLFQEPAPRQSEPDVTRKT 301
Db 243 MEGFNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETWNRSLFQEPAPRQSEPDVTRKT 302
QY 302 PDYFL 306
Db 303 PDYFL 307

RESULT 5
T03389
probable phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03389
R/Chang, M.C.; Chen, X.; Wang, B.
submitted to the EMBL Data Library, February 1996
A/Reference number: Z14920
A/Accession: T03389
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-306 <CHA>
A/Cross-references: UNIPROT:Q42981; UNIPARC:UPI00000A2648; EMBL:U49113; NID:G1218053; PI
A/Experimental source: seed, strain IR36
C/Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosph
C/Keywords: phosphoric monoester hydrolase
F:20-279/Domain: phosphoprotein phosphatase homology <PPP>
F:48-116/Domain: phosphoesterase core homology <PEC>

Query Match 88.7%; Score 1481; DB 2; Length 306;
Best Local Similarity 86.3%; Pred. No. 2.4e-124;
Matches 264; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEMNVQPKCPVT 60
Db 1 MPSHADLRQISURECKPLGEAEVRAJCEQAKAILMEEMNVQPKCPVT 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVKKVYRDLTILRGNHESRQI 120
Db 61 DLIELFRIGGSDPDNTNLFMGDYVDRGYYSVETVSLVALLVKKVYRDLTILRGNHESRQI 120
QY 121 TVQVGFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRAL 180
Db 121 TVQVGFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRAL 180
QY 181 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
Db 181 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
QY 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETWNRSLFQEPAPRQSEPDVTRK 300
Db 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETWNRSLFQEPAPRQSEPDVTRK 300
QY 301 PDYFL 306
Db 301 PDYFL 306

RESULT 6
T03599
phosphoprotein phosphatase (EC 3.1.3.16) 2A, npp4 - common tobacco
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
C/Accession: T03599
R/Suh, M.; Cho, H.; Kim, Y.; Liu, J.; Lee, H.
Plant Mol. Biol. 36, 315-322, 1998
A/Title: Multiple genes encoding serine/threonine protein phosph
A/Reference number: Z14967; MUID:98145437; PMID:9484443
A/Accession: T03599
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-302 <SUH>
A/Cross-references: UNIPROT:O04859; UNIPARC:UPI00000A0317; EMBL:
A/Experimental source: cultivar Xanth
C/Genetics:
A/Gene: npp4
C/Superfamily: serine/threonine protein phosphatase; phosphoeste
C/Keywords: iron; phosphoric monoester hydrolase; serine/threoni
F:18-275/Domain: phosphoprotein phosphatase homology <PPP>
F:44-112/Domain: phosphoesterase core homology <PEC>

Query Match 86.5%; Score 1445; DB 2; Length 302
Best Local Similarity 86.3%; Pred. No. 3.8e-121;
Matches 264; Conservative 17; Mismatches 21; Indels

QY 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEMNVQPKCPVT 60
Db 1 MPSHG--DRQIAQLMECKPLSEAEVKTLCDQAGTV--RMNVQPKCPVT 56
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVKKVYRDLTIL 120
Db 57 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALLVKKVYRDLTIL 116
QY 121 TVQVGFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPS 180
Db 117 TVQVGFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPS 176
QY 181 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNG 240
Db 177 RQIEVPHEGPMCDLLWSDDPDRCGWISPRGAGYTFGQDIAEQFNHTNG 236
QY 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETWNRSLFQEPAP 300
Db 237 VMDGFNWCQDKNVVTVFSPAPNYCYRCGNMAAILEIGENLQNFLOFDP 296
QY 301 TPDYFL 306
Db 297 TPDYFL 302

RESULT 7
A27430
phosphoprotein phosphatase (EC 3.1.3.16) 2-alpha catalytic chain
A/Alternate names: phosphoprotein phosphatase 2A-alpha catalytic
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
C/Accession: A27430
R/Stone, S.R.; Hofsteenge, J.; Hemmings, B.A.
Biochemistry 26, 7215-7220, 1987
A/Title: Molecular cloning of cDNAs encoding two isoforms of the
A/Reference number: A27430; MUID:88107662; PMID:2827745
A/Accession: A27430
A/Molecule type: mRNA
A/Residues: 1-309 <STO>
A/Cross-references: UNIPROT:P05323; UNIPARC:UPI0000000C15; GB:M2
C/Superfamily: serine/threonine protein phosphatase; phosphoeste
C/Keywords: iron; metalloprotein; phosphoric monoester hydrolase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His) #status
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predict

Query Match 85.4%; Score 1427; DB 1; Length 305

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Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

QY 6 DVDROIQLSECKPLSELEVNKLCQARTILVEENNVQPKPVTVCGIHQFHDILIEL 65
   :::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESQVKSCLCEKAKEILTKESNVQEVRCPTVCQFHDIMEL 68
   :::::::::::::::::::::
QY 66 FRIGKAPDTNLYFMGDYVDGRGYYSVETVSLVALVKVRYRDRITILRGHESRQITQYVG 125
   :::::::::::::::::::::
Db 69 FRIGKSPDTNLYFMGDYVDGRGYYSVETVTLVALVKVRYRERITILRGHESRQITQYVG 128
   :::::::::::::::::::::
QY 126 FYDECLRYKYGANVWKYFTDLFDYPLPLTALIEHEIFCLHGGLSPSLTDLRDRLQ 185
   :::::::::::::::::::::
Db 129 FYDECLRYKYGANVWKYFTDLFDYPLPLTALVQGIQFCLHGGLSPSIDILDRDRLQ 188
   :::::::::::::::::::::
QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVARAQLVMEGY 245
   :::::::::::::::::::::
Db 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNHANGLLTIVSRAQLVMEGY 248
   :::::::::::::::::::::
QY 246 NWCQDNVTVFSAFNPCYRCGNMAAIMEIDTMNRSFLOPEPAPRQSEPDVTRTPDYF 305
   :::::::::::::::::::::
Db 249 NWCHDRNVVTFSAFNPCYRCGNQAAIMELDDTLKYSFLQFDPAPRGPGEHVTRTPDYF 308
   :::::::::::::::::::::
QY 306 L 306
Db 309 L 309

RESULT 8
PAHU2A
phosphoprotein phosphatase (EC 3.1.3.16) 2-alpha catalytic chain - human
N:Alternate names: phosphoprotein phosphatase 2A-alpha catalytic chain; protein phosphat
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 05-Oct-2004
C:Accession: S011986; A37135; A32143
R:Stone, S.R.; Mayer, R.; Wernet, W.; Maurer, F.; Hofsteenge, J.; Hemmings, B.A.
Nucleic Acids Res. 16, 11365, 1988
A:Title: The nucleotide sequence of the cDNA encoding the human lung protein phosphatase
A:Reference number: S01986; MUID:89083567; PMID:2849764
A:Accession: S01986
A:Molecule type: mRNA
A:Residues: 1-309 <STO>
A:Cross-references: UNIPROT:P05323; UNIPARC:UPI00000000C15; EMBL:X12646; NID:G36119; PIDN
R:Knew-Goodall, Y.; Mayer, R.E.; Maurer, F.; Stone, S.R.; Hemmings, B.A.
Biochemistry 30, 89-97, 1991
A:Title: Structure and transcriptional regulation of protein phosphatase 2A catalytic su
A:Reference number: A37135; MUID:91105105; PMID:1846293
A:Accession: A37135
A:Molecule type: DNA
A:Residues: 1-309 <KHE>
A:Cross-references: UNIPARC:UPI00000000C15; GB:M60483; GB:J05297; NID:G190223; PIDN:AAA36
R:Arino, J.; Woon, C.W.; Brautigan, D.L.; Miller Jr., T.B.; Johnson, G.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 4252-4256, 1988
A:Title: Human liver phosphatase 2A: cDNA and amino acid sequence of two catalytic subun
A:Reference number: A94200; MUID:88248000; PMID:2837763
A:Accession: A32143
A:Molecule type: mRNA
A:Residues: 1-309 <ARI>
A:Cross-references: UNIPARC:UPI00000000C15; GB:J03804; NID:G1707870; PIDN:AAB38019.1; PID
A:Experimental source: liver; clone HL-14
A>Note: the authors translated the codon CAT for residue 63 as Glu
C:Genetics:
A:Gene: GDB:PPP2CA
A:Cross-references: GDB:126878; OMIM:176915
A:Map position: 5q23.2-5q31.2
C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predicted

```

```

Query Match 85.4%; Score 1427; DB 1; Length 309
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDROIQLSECKPLSELEVNKLCQARTILVEENNVQPKPVTVCGIHQFHDILIEL 65
   :::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESQVKSCLCEKAKEILTKESNVQEVRCPTVCQFHDIMEL 68
   :::::::::::::::::::::
QY 66 FRIGKAPDTNLYFMGDYVDGRGYYSVETVSLVALVKVRYRDRITILRGHESRQITQYVG 125
   :::::::::::::::::::::
Db 69 FRIGKSPDTNLYFMGDYVDGRGYYSVETVTLVALVKVRYRERITILRGHESRQITQYVG 128
   :::::::::::::::::::::
QY 126 FYDECLRYKYGANVWKYFTDLFDYPLPLTALIEHEIFCLHGGLSPSLTDLRDRLQ 185
   :::::::::::::::::::::
Db 129 FYDECLRYKYGANVWKYFTDLFDYPLPLTALVQGIQFCLHGGLSPSIDILDRDRLQ 188
   :::::::::::::::::::::
QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVAL 245
   :::::::::::::::::::::
Db 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNHANGLLTIVS 248
   :::::::::::::::::::::
QY 246 NWCQDNVTVFSAFNPCYRCGNMAAIMEIDTMNRSFLOPEPAPRQSEPDVTRTPDYF 305
   :::::::::::::::::::::
Db 249 NWCHDRNVVTFSAFNPCYRCGNQAAIMELDDTLKYSFLQFDPAPRGPGEHVTRTPDYF 308
   :::::::::::::::::::::
QY 306 L 306
Db 309 L 309

```

```

RESULT 9
PARB1
phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 0
C:Accession: S00104; S18812; A60240
R:da Cruz e Silva, O.B.; Alamy, S.; Campbell, D.G.; Cohen, P.T.
FEBS Lett. 221, 415-422, 1987
A:Title: Isolation and sequence analysis of a cDNA clone encoding
A:Reference number: S00104; MUID:87304854; PMID:3040474
A:Accession: S00104
A:Molecule type: mRNA
A:Residues: 1-309 <DAC>
A:Cross-references: UNIPROT:P05323; UNIPARC:UPI00000000C15; EMBL:
A:Accession: S18812
A:Molecule type: protein
A:Residues: 9-21;67-80;215-229,'X',231-238;277-298;304-308 <DAC2
A:Cross-references: UNIPARC:UPI00001727FF; UNIPARC:UPI0000172800
R:Stone, S.R.; Hofsteenge, J.; Hemmings, B.A.
Adv. Exp. Med. Biol. 231, 559-566, 1988
A:Title: Primary structure of protein phosphatase 2A as determin
A:Reference number: A60240; MUID:88323941; PMID:2843014
A:Accession: A60240
A:Molecule type: protein
A:Residues: 2-19;26-37;48-62,'X',64-87;137-144;186-190,'X',192-1
A:Cross-references: UNIPARC:UPI0000172804; UNIPARC:UPI0000172805
C:Superfamily: serine/threonine protein phosphatase; phosphoeste
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predict

```

```

Query Match 85.4%; Score 1427; DB 1; Length 309
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDROIQLSECKPLSELEVNKLCQARTILVEENNVQPKPVTVCGIHQFHDILIEL 65
   :::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESQVKSCLCEKAKEILTKESNVQEVRCPTVCQFHDIMEL 68
   :::::::::::::::::::::

```

```

QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVALVKVRYDRITILRGNE 125
DB 69 FRIGKSPDNTYLFMGDYVDRGYYSVEITVLLVALVKVRYRERITILRGNE 128
QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLDITLC 185
DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDITLC 188
QY 186 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDIAEQFNHTNGLSLVA 245
DB 189 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDISETFNHANGLLTIVE 248
QY 246 NWCODKNVTVFSAFNVCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEI 305
DB 249 NWCHDRNVTVFSAFNVCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEE 308
QY 306 L 306
DB 309 L 309

RESULT 10
PART2A
phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 05-Oct-2004
C:Accession: S06592; J50060; F50311; A36491
R:Posas, F.; Arino, J.
Nucleic Acids Res. 17, 8369, 1989
A:Title: Nucleotide sequence of a rat heart cDNA encoding the isotype alpha of the catalytic subunit of phosphoprotein phosphatase
A:Reference number: S06592; MUID:90045961; PMID:2554255
A:Accession: S06592
A:Molecule type: mRNA
A:Residues: 1-309 <POS>
A:Cross-references: UNIPROT:P13353; UNIPARC:UPI0000001961; EMBL:X16043; NID:G56818; PIDN:K16043; NID:G56818; PIDN:K16043; NID:G56818
R:Kitagawa, Y.; Tahira, T.; Ikeda, I.; Kikuchi, K.; Tsuki, S.; Sugimura, T.; Nagao, M.
Biochim. Biophys. Acta 951, 123-129, 1988
A:Title: Molecular cloning of cDNA for the catalytic subunit of rat liver type 2A protein
A:Reference number: J50060; MUID:89051001; PMID:2461222
A:Accession: J50060
A:Molecule type: mRNA
A:Residues: 1-309 <KIT>
A:Cross-references: UNIPARC:UPI0000001961; GB:M33114; NID:G206286; PIDN:AAA41904.1; PID:AAA41904.1
A:Accession: P50311
A:Molecule type: protein
A:Residues: 284, 'P', 286-289, 'L', 291-293 <KIT>
A:Cross-references: UNIPARC:UPI000017280B
R:Wadzinski, B.E.; Heasley, L.E.; Johnson, G.L.
J. Biol. Chem. 265, 21504-21508, 1990
A:Title: Multiplicity of protein serine-threonine phosphatases in PC12 pheochromocytoma
A:Reference number: A36491; MUID:91072341; PMID:2174876
A:Accession: A36491
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 204-260 <WAD>
A:Cross-references: UNIPARC:UPI000000049B; GB:M58438; NID:G206300; PIDN:AAA41911.1; PID:AAA41911.1
C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphatase; iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57-59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 85.4%; Score 1427; DB 1; Length 309;
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

QY 6 DVDRQIEQLSECKPLSELVKNLDCQARTILVEENNVQPKVPCVTVCDDI 65
DB 9 ELDQWIEQLNECKQLSESVQKSLCEKAKEILTKESNVQEVRCPTVTCGDV 68
QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVALVKVRYDRITILRGNE 125
DB 69 FRIGKSPDNTYLFMGDYVDRGYYSVEITVLLVALVKVRYRERITILRGNE 128
QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLDITLC 185
DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDITLC 188
QY 186 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDIAEQFNHTNGLSLVA 245
DB 189 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDISETFNHANGLLTIVE 248
QY 246 NWCODKNVTVFSAFNVCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEI 305
DB 249 NWCHDRNVTVFSAFNVCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEE 308
QY 306 L 306
DB 309 L 309

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QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVALVKVRYDRITILRGNE 125
DB 69 FRIGKSPDNTYLFMGDYVDRGYYSVEITVLLVALVKVRYRERITILRGNE 128
QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLDITLC 185
DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDITLC 188
QY 186 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDIAEQFNHTNGLSLVA 245
DB 189 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDISETFNHANGLLTIVE 248
QY 246 NWCODKNVTVFSAFNVCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEI 305
DB 249 NWCHDRNVTVFSAFNVCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEE 308
QY 306 L 306
DB 309 L 309

RESULT 11
S10371
phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 004
C:Accession: S10371; S32226
R:de Paoli-Roach, A.A.
Submitted to the EMBL Data Library, March 1990
A:Description: Nucleotide sequence of a cDNA encoding the protein
A:Reference number: S10371
A:Accession: S10371
A:Molecule type: mRNA
A:Residues: 1-309 <DSP>
A:Cross-references: UNIPROT:P05323; UNIPARC:UPI00000000C15; EMBL:U00000000C15; NID:G628; PIDN:G628; PIDN:G628
R:Chen, S.; Boynton, A.
Submitted to the EMBL Data Library, March 1993
A:Description: Nucleotide sequence of a bovine brain cDNA encoding the protein
A:Reference number: S32226
A:Accession: S32226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-309 <CHE>
A:Cross-references: UNIPARC:UPI00000000C15; EMBL:X72858; NID:G28E
A:Experimental source: brain
C:Superfamily: serine/threonine protein phosphatase; phosphoesterase
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57-59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 85.4%; Score 1427; DB 1; Length 309;
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDRQIEQLSECKPLSELVKNLDCQARTILVEENNVQPKVPCVTVCDDI 65
DB 9 ELDQWIEQLNECKQLSESVQKSLCEKAKEILTKESNVQEVRCPTVTCGDV 68
QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVALVKVRYDRITILRGNE 125
DB 69 FRIGKSPDNTYLFMGDYVDRGYYSVEITVLLVALVKVRYRERITILRGNE 128
QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLDITLC 185
DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDITLC 188
QY 186 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDIAEQFNHTNGLSLVA 245
DB 189 VPHEGPMCDLLWSDDDRCGWGISPRGAGYTFQDISETFNHANGLLTIVE 248
QY 246 NWCODKNVTVFSAFNVCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEI 305
DB 249 NWCHDRNVTVFSAFNVCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEE 308
QY 306 L 306
DB 309 L 309

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A:Reference number: A94200; MUID:88248000; PMID:2837763

A:Accession: B32143

A:Molecule type: mRNA

A:Residues: 2-18, D', 20-309 <AR2>

A:Cross-references: UNIPARC:UPI000016A537; GB:J03805; NID:gl178437; PIDN:AAB38020.1; PID:

A:Experimental source: liver; clone HL-1

A>Note: the authors translated the codon GAC for residue 18 as Glu

R:Virshup, D.M.; Kauffman, M.G.; Kelly, T.J.

EMBO J. 8, 3891-3898, 1989

A:Title: Activation of SV40 DNA replication in vitro by cellular protein phosphatase 2A.

A:Reference number: S09378; MUID:90059993; PMID:2555176

A:Accession: S09378

A:Molecule type: protein

A:Residues: 91-97;111-114;122-127;137-144;207-238 <VIR>

A:Cross-references: UNIPARC:UPI0000172807; UNIPARC:UPI000017280C; UNIPARC:UPI000017280D;

R:Pallas, D.C.; Shahrak, L.K.; Martin, B.L.; Jaspers, S.; Miller, T.B.; Brautigan, D.L.;

Cell 60, 167-176, 1990

A:Title: Polyoma small and middle T antigens and SV40 small t antigen form stable complex

A:Reference number: A34060; MUID:90106638; PMID:2153055

A:Accession: A34060

A:Molecule type: protein

A:Residues: 75-89;215-234;X', 270-294;303-309 <PAL>

A:Cross-references: UNIPARC:UPI0000172810; UNIPARC:UPI0000172811; UNIPARC:UPI0000172812;

C:Genetics: GDB:PPP2CB

A:Gene: GDB:PPP2CB

A:Cross-references: GDB:126879; OMIM:176916

A:Map position: 8p12-8p11.2

C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phospho

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted

F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His)

F:88,118,265/Active site: Asp, His, Tyr #status predicted

F:89,214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 84.5%; Score 1411; DB 1; Length 309;

Best Local Similarity 82.4%; Pred. No. 4.2e-118;

Matches 248; Conservative 34; Mismatches 19; Indels 0; Gaps 0;

QY 6 DVDRIEQLSECKPLSELEVNKLCQARTILVEEWNVPVKCPVTVCGDI 65

Db 9 ELDQWVEQLNECKQLNENQVRLTCEKAKEILTKESNVQEVRCVPVTVCGDV 68

QY 66 FRIGKAPDTNLYFMGDIYVDRGYYSVETVLLVALVKVRYDRITILRGNE 125

Db 69 FRIGKSPDTNLYFMGDIYVDRGYYSVETVLLVALVKVRYPERITILRGNE 128

QY 126 FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDTRIQE 185

Db 129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDTLDHIALDLRQ 188

QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLVMEGY 245

Db 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGITLVSAHQLVMEGY 248

QY 246 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPROSEPDVTRKTPDYF 305

Db 249 NWCHDRNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPROSEPDVTRKTPDYF 308

QY 306 L 306

Db 309 L 309

RESULT 15

PARB2B

phosphoprotein phosphatase (EC 3.1.3.16) 2A-beta catalytic chain - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004

C:Accession: S00220

R:da Cruz e Silva, O.B.; Cohen, P.T.W.

FEBS Lett. 226, 176-178, 1987

A:Title: A second catalytic subunit of type-2A protein phosphatase

A:Reference number: S00220; MUID:88083628; PMID:2826253

A:Accession: S00220

A:Molecule type: mRNA

A:Residues: 1-309 <DA1>

A:Cross-references: UNIPROT:P11611; UNIPARC:UPI0000130FC8; EMBL:

C:Superfamily: serine/threonine protein phosphatase; phosphoesterase

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted

F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His)

F:88,118,265/Active site: Asp, His, Tyr #status predicted

F:89,214/Binding site: substrate phosphate (Arg) #status predict

Query Match 84.5%; Score 1411; DB 1; Length 309

Best Local Similarity 82.4%; Pred. No. 4.2e-118;

Matches 248; Conservative 34; Mismatches 19; Indels

QY 6 DVDRIEQLSECKPLSELEVNKLCQARTILVEEWNVPVKCPVTVCGDI 65

Db 9 ELDQWVEQLNECKQLNENQVRLTCEKAKEILTKESNVQEVRCVPVTVCGDV 68

QY 66 FRIGKAPDTNLYFMGDIYVDRGYYSVETVLLVALVKVRYDRITILRGNE 125

Db 69 FRIGKSPDTNLYFMGDIYVDRGYYSVETVLLVALVKVRYPERITILRGNE 128

QY 126 FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDTRIL 185

Db 129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDTLL 188

QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVA 245

Db 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGITLVE 248

QY 246 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPROSEEE 305

Db 249 NWCHDRNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPRGEE 308

QY 306 L 306

Db 309 L 309

Search completed: December 9, 2005, 10:24:08

Job time : 41 secs

rabbit skeletal n

NID:gl1684; PIDN:C
e homology; phosph
/threonine-specif

ed

s 0;

EL 65

EL 68

YG 125

YG 128

QE 185

QE 188

GY 245

GY 248

YF 305

YF 308

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:13:51 ; Search time 46 Seconds
(without alignments)
549.973 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MPSVADVDRIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1670	100.0	306	2	US-09-828-302-13
2	1427	85.4	309	2	US-09-538-092-854
3	1427	85.4	355	2	US-09-949-016-11414
4	1411	84.5	309	2	US-09-538-092-902
5	1411	84.5	309	2	US-09-949-016-6461
6	1411	84.5	311	2	US-09-949-016-11335
7	1326	79.4	325	2	US-09-190-976B-10
8	1291	77.3	377	2	US-09-487-558B-270
9	1286	77.0	369	2	US-09-487-558B-268
10	1137.5	68.1	341	2	US-09-949-016-8780
11	973	58.3	312	2	US-09-949-016-9733
12	963.5	57.7	318	2	US-09-248-796A-18310
13	942.5	56.4	303	2	US-09-916-338A-2
14	786	47.1	271	2	US-09-248-796A-18309
15	757	45.3	323	2	US-09-538-092-1093
16	756	45.3	312	2	US-09-538-092-256
17	739	44.3	330	2	US-09-167-206-6
18	739	44.3	330	2	US-09-538-092-873
19	739	44.3	374	2	US-09-949-016-7363
20	736	44.1	327	2	US-09-538-092-1095
21	736	44.1	327	2	US-09-949-016-6266
22	736	44.1	356	2	US-09-949-016-8084
23	731	43.8	330	2	US-09-190-976B-8
24	729.5	43.7	319	2	US-09-248-796A-18323
25	696.5	41.7	260	2	US-09-248-796A-18344
26	639	38.3	184	2	US-09-248-796A-18313
27	629.5	37.7	692	2	US-09-487-558B-274

28	614.5	36.8	710	2	US-09-487-558B-276	Sequ
29	565	33.8	502	2	US-09-949-016-10218	Sequ
30	565	33.8	510	2	US-09-744-016A-6	Sequ
31	565	33.8	521	2	US-09-538-092-1283	Sequ
32	565	33.8	523	2	US-09-744-016A-21	Sequ
33	565	33.8	533	2	US-09-744-016A-18	Sequ
34	559	33.5	487	1	US-08-452-722-7	Sequ
35	559	33.5	487	1	US-08-404-731A-7	Sequ
36	559	33.5	487	1	US-08-344-237-7	Sequ
37	559	33.5	487	1	US-08-503-226B-7	Sequ
38	559	33.5	487	2	US-08-721-458B-7	Sequ
39	559	33.5	528	2	US-09-744-016A-9	Sequ
40	559	33.5	530	2	US-09-949-016-11683	Sequ
41	559	33.5	535	2	US-09-744-016A-24	Sequ
42	543	32.5	499	2	US-09-949-016-7370	Sequ
43	540	32.3	553	2	US-09-744-016A-27	Sequ
44	539.5	32.3	502	2	US-09-949-016-6642	Sequ
45	539.5	32.3	509	2	US-09-744-016A-12	Sequ

ALIGNMENTS

RESULT 1
US-09-828-302-13
; Sequence 13, Application US/09828302
; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND V
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-302-13

Query Match	100.0%	Score 1670;	DB 2;	Length 30
Best Local Similarity	100.0%	Pred. No. 1.9e-178;		
Matches 306;	Conservative 0;	Mismatches 0;	Indels	
Qy	1	MPSVADVDRIEQLSECKPLSEVKNLCOARTILVEENNVQPKCPVT		1PH 60
Db	1	MPSVADVDRIEQLSECKPLSEVKNLCOARTILVEENNVQPKCPVT		1PH 60
Qy	61	DLIELFRIGGKAPDTNLYFMGDYVDGRGYSVETVSLVALKVRDRITTI		QI 120
Db	61	DLIELFRIGGKAPDTNLYFMGDYVDGRGYSVETVSLVALKVRDRITTI		QI 120
Qy	121	TQVYGFYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGLSPS		AL 180
Db	121	TQVYGFYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGLSPS		AL 180
Qy	181	DRIVEPHEGPMCDLLMSDDPDRCGWGISPRGAGYTFQODIAEQPHNTNC		QL 240
Db	181	DRIVEPHEGPMCDLLMSDDPDRCGWGISPRGAGYTFQODIAEQPHNTNC		QL 240
Qy	241	VMGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDTMNRSFLQFEPAF		RK 300
Db	241	VMGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDTMNRSFLQFEPAF		RK 300
Qy	301	TPDYFL 306		

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Db          301 TPDYFL 306

RESULT 2
US-09-538-092-854
; Sequence 854, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 854
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P05323
US-09-538-092-854

Query Match      85.4%; Score 1427; DB 2; Length 309;
Best Local Similarity 83.7%; Pred. No. 3.3e-151;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVLEENNVQPKVPCVTCGDHDLIEL 65
      :::::::::::::::::::::
Db      9 ELDQWIEQLNECKQLSESVKSLCEKAKEILTKESNVQEVRCPTVCGDVHGHDLNEL 68
      :::::::::::::::::::::

Qy      66 FRIGKAPDPTNYLFMGDYVDRGYYSVETVSLVALLVAKVRYRDRITILRGNHESRQITQVYG 125
      :::::::::::::::::::::
Db      69 FRIGKSPDPTNYLFMGDYVDRGYYSVETVTLVALLVAKVRYRDRITILRGNHESRQITQVYG 128
      :::::::::::::::::::::

Qy      126 FYDECLRKYGNANWKYFTDLFDYLPALTALTEHEIFCLHGLSPSLDTHLRALDRLOE 185
      :::::::::::::::::::::
Db      129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGLSPSIDTLHRALDRLOE 188
      :::::::::::::::::::::

Qy      186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEFNHTNGLSLVARAHQLVMEGY 245
      :::::::::::::::::::::
Db      189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGTLVLSRAHQLVMEGY 248
      :::::::::::::::::::::

Qy      246 NWCQDKNVVTFSPAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
      :::::::::::::::::::::
Db      249 NWCHDRNVVTFSPAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRGEPHVRTPTDYF 308
      :::::::::::::::::::::

Qy      306 L 306
      |
Db      309 L 309

RESULT 3
US-09-949-016-11414
; Sequence 11414, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11414
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11414

Query Match      85.4%; Score 1427; DB 2; Length 355
Best Local Similarity 83.7%; Pred. No. 4.1e-151;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVLEENNVQPKVPCVTCGDHDLIEL 65
      :::::::::::::::::::::
Db      55 ELDQWIEQLNECKQLSESVKSLCEKAKEILTKESNVQEVRCPTVTCGDV 114
      :::::::::::::::::::::

Qy      66 FRIGKAPDPTNYLFMGDYVDRGYYSVETVSLVALLVAKVRYRDRITILRGNH 125
      :::::::::::::::::::::
Db      115 FRIGKSPDPTNYLFMGDYVDRGYYSVETVTLVALLVAKVRYRDRITILRGNH 174
      :::::::::::::::::::::

Qy      126 FYDECLRKYGNANWKYFTDLFDYLPALTALTEHEIFCLHGLSPSLDTHLRALDRLOE 185
      :::::::::::::::::::::
Db      175 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGLSPSIDTLHRALDRLOE 234
      :::::::::::::::::::::

Qy      186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEFNHTNGLSLVARAHQLVMEGY 245
      :::::::::::::::::::::
Db      235 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGTLVLSRAHQLVMEGY 294
      :::::::::::::::::::::

Qy      246 NWCQDKNVVTFSPAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
      :::::::::::::::::::::
Db      295 NWCHDRNVVTFSPAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRGEPHVRTPTDYF 354
      :::::::::::::::::::::

Qy      306 L 306
      |
Db      355 L 355

RESULT 4
US-09-538-092-902
; Sequence 902, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of U
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 902
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P11082
US-09-538-092-902

Query Match      84.5%; Score 1411; DB 2; Length 309
Best Local Similarity 82.4%; Pred. No. 2e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVLEENNVQPKVPCVTCGDHDLIEL 65
      :::::::::::::::::::::
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Db 9 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVTCGDVHGQFHDLMEL 68
QY 66 FRIGKAPDNTYLFMGDVYDRGYSVETVLLVALKVRYDRITTLRGHESRQITQYVG 125
Db 69 FRIGKSPDNTYLFMGDVYDRGYSVETVLLVALKVRYPERITTLRGHESRQITQYVG 128
QY 126 FYDECLRKYGNANWKYFTDLFDYLLPLTALIEHEIFCLHGGLSPLSLDTHIRALDRIOE 185
Db 129 FYDECLRKYGNANWKYFTDLFDYLLPLTALVDCQIFCLHGGLSPLSLDTHIRALDRIOE 188
QY 186 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLWMEGY 245
Db 189 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDISETFNANGILTVSRAHQLWMEGY 248
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
Db 249 NWCHDRNVTVFSAPNYCYRCGNQAAIMELDDTLKYSFLQDPAPRGPETHVTRTPDYF 308
QY 306 L 306
Db 309 L 309
RESULT 5
US-09-949-016-6461
; Sequence 6461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6461
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6461
Query Match 84.5%; Score 1411; DB 2; Length 309;
Best Local Similarity 82.4%; Pred. No. 2e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0; Gaps 0;
QY 6 DVDRIEQLSECKPLSELEVNLCDOARTILVEENVQVPCVTCGDIHGQFHDLMEL 65
Db 9 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVTCGDVHGQFHDLMEL 68
QY 66 FRIGKAPDNTYLFMGDVYDRGYSVETVLLVALKVRYDRITTLRGHESRQITQYVG 125
Db 69 FRIGKSPDNTYLFMGDVYDRGYSVETVLLVALKVRYPERITTLRGHESRQITQYVG 128
QY 126 FYDECLRKYGNANWKYFTDLFDYLLPLTALIEHEIFCLHGGLSPLSLDTHIRALDRIOE 185
Db 129 FYDECLRKYGNANWKYFTDLFDYLLPLTALVDCQIFCLHGGLSPLSLDTHIRALDRIOE 188
QY 186 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLWMEGY 245
Db 189 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDISETFNANGILTVSRAHQLWMEGY 248
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
Db 249 NWCHDRNVTVFSAPNYCYRCGNQAAIMELDDTLKYSFLQDPAPRGPETHVTRTPDYF 308
QY 306 L 306

Db 309 L 309
RESULT 6
US-09-949-016-11335
; Sequence 11335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11335
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11335
Query Match 84.5%; Score 1411; DB 2; Length 311
Best Local Similarity 82.4%; Pred. No. 2.1e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0;
QY 6 DVDRIEQLSECKPLSELEVNLCDOARTILVEENVQVPCVTCGDI 65
Db 11 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVTCGDV 70
QY 66 FRIGKAPDNTYLFMGDVYDRGYSVETVLLVALKVRYDRITTLRGH 125
Db 71 FRIGKSPDNTYLFMGDVYDRGYSVETVLLVALKVRYPERITTLRGH 130
QY 126 FYDECLRKYGNANWKYFTDLFDYLLPLTALIEHEIFCLHGGLSPLSLD 185
Db 131 FYDECLRKYGNANWKYFTDLFDYLLPLTALVDCQIFCLHGGLSPLSLD 190
QY 186 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVA 245
Db 191 VPHEGPMCDLLWSDDRCGNGISPRGAGYTFGQDISETFNANGILTV 250
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSE 305
Db 251 NWCHDRNVTVFSAPNYCYRCGNQAAIMELDDTLKYSFLQDPAPRGE 310
QY 306 L 306
Db 311 L 311
RESULT 7
US-09-190-976B-10
; Sequence 10, Application US/09190976B
; Patent No. 6815187
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Horowitz, Arie
; TITLE OF INVENTION: Stimulation of angiogenesis via
; syndecan-4 cytoplasmic domain signa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Frashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
hway

```

; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 270
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-487-558B-270

Query Match 77.3%; Score 1291; DB 2; Length 377
Best Local Similarity 76.3%; Pred. No. 7.9e-136;
Matches 229; Conservative 34; Mismatches 37; Indels

QY 7 VDRQIEQLSECKPLSELEVKNICDQARTILVSENNVQPKPVTTCGDIIH
|F 66
||
|F 137
|F 126
|F 197
|F 186
|F 257
|F 246
|F 317
|F 306
|F 377

; RESULT 9
; US-09-487-558B-268
; Sequence 268, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-487-558B-268

Query Match 77.0%; Score 1286; DB 2; Length 369
Best Local Similarity 75.7%; Pred. No. 2.8e-135;
Matches 227; Conservative 35; Mismatches 38; Indels

QY 7 VDRQIEQLSECKPLSELEVKNICDQARTILVSENNVQPKPVTTCGDIIH
|F 66

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Db 70 LDQWIEHLSKCEPLSEDDVARLCKMAVDVLQFEENVKPINVPVTCIGDVHGQFHDLLLELF 129
Qy 67 RIGGKAPDNYLFMGDYVDRGYVETVSVLLVALKVRYDRDRTITILRGHSHESQITQVYGF 126
Db 130 KIGGPCPDNYLFMGDYVDRGYVETVSVLYAMKVRYPHRITILRGHSHESQITQVYGF 189
Qy 127 YDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSPSLDTHIRALDRIOEV 186
Db 190 YDECLRKYGNAVWKMTDLFDYFPITALVDNKFCLHGGSPMETIDQVRELARIQEV 249
Qy 187 PHEGPMCDLLWSDDPDRCGWISPRGAGYTFQODIABQFNHTNGLSVARAHQLWEGYN 246
Db 250 PHEGPMCDLLWSDDPDRCGWISPRGAGTFQODVSEQFNHTNGLSVARAHQLWEGYA 309
Qy 247 WCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEFAPRQSPDVTTRKTPDYFL 306
Db 310 WSHQONVTVTFSAPNYCYRCGNMAAIMEVDENHNKQFLQYDPSVRGPSPSRKTPDYFL 369

RESULT 10
US-09-949-016-8780
; Sequence 8780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8780
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8780
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Query Match 68.1%; Score 1137.5; DB 2; Length 341;
Best Local Similarity 66.4%; Pred. No. 1.1e-118;
Matches 204; Conservative 46; Mismatches 56; Indels 1; Gaps 1;

Qy 1 MPSVADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKVPTVCGDIHQGFH 60
Db 35 MAEISDLDRQIEQLRCELKESEVKALCAKAREILVEESNVQRVDSPTVCGDIHQGFY 94

Qy 61 DLIELFRIGKAPDNYLFMGDYVDRGYVETVSVLLVALKVRYDRDRTITILRGHSHESQI 120
Db 95 DLKELFRVGGDVPETNYLFMGDYVDRGYVETVSVLLVALKVRYDRDRTITILRGHSHESQI 154

Qy 121 TVQVGYFDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSPSLDTHIRAL 180
Db 155 TVQVGYFDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSPSLDTHIRAL 214

Qy 181 DRIQVHPHEGPMCDLLWSDDPDRCGWISPRGAGYTFQODIABQFNHTNGLSVARAHQL 240
Db 215 DRKQVHPHGGPMCDLLWSDDPDRCGWISPRGAGYTFQODIABQFNHTNGLSVARAHQL 274

Qy 241 VMGYNWQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEFAPRQSPDVTTRK 300
Db 275 VMGYNWQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEFAPRQSPDVTTRK 334

Qy 301 -TPDYFL 306
Db 335 PVADYFL 341
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RESULT 11
US-09-949-016-9733
; Sequence 9733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9733
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9733

Query Match 58.3%; Score 973; DB 2; Length 312;
Best Local Similarity 58.8%; Pred. No. 2.6e-100;
Matches 177; Conservative 41; Mismatches 83; Indels 0;

Qy 6 DVDRIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKVPTVCGDI 65
Db 12 DLKYEIARLCKYLPENDLARKLCYVCDLLEESNVQPVSTPTVCGDI 71

Qy 66 PRIGKAPDNYLFMGDYVDRGYVETVSVLLVALKVRYDRDRTITILRGH 125
Db 72 FRTGGQVPTNYIFMGDFVDRGYVETVSVLLVALKVRYDRDRTITILRGH 131

Qy 126 FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSPSLDTHI 185
Db 132 FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSPSLDTHI 191

Qy 186 VPHEGPMCDLLWSDDPDRCGWISPRGAGYTFQODIABQFNHTNGLSVLA 245
Db 192 IPHKGAFCDLVSDPEDVDVTWAIISPRGAGWLFQAKVTFVHINNKLIC 251

Qy 246 NWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEFAPRQSEF 305
Db 252 KFMFDEKLVTVWSAPNYCYRCGNIAIMVFKDVNTREPKLFRVAPDSRV 311

Qy 306 L 306
Db 312 L 312

RESULT 12
US-09-248-796A-18310
; Sequence 18310, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
; ATED TO THE DIAGNOSIS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18310
; LENGTH: 318
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CANDIDA ALBICANS

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1093
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P36873
US-09-538-092-1093

Query Match	45.3%	Score 757;	DB 2;	Length 323;
Best Local Similarity	46.3%	Pred. No. 4.6e-76;		
Matches 142;	Conservative 66;	Mismatches 87;	Indels 12;	Gaps 6;

Qy	6	DVDRIEQLSE---CKP-----LSLEVNLCDAQARTILVSEWNPVKCPVTVCDDIHG	57
Db	8	NIDSIQRLLEVRGSKPGKNVQLQENEIRGLCKSRFISQPIILLEAPLKICGDIHG	67
Qy	58	QPHDLIELPRIGGKAPDTNYLFMGDYVDRGYVSVETSLVALKVYRDRITILRGNHES	117
Db	68	QYDILLRLEFYGGPPESNYLPLGDYVDRGQSLEIICLLAYKIKYPENFLLRGHEC	127
Qy	118	RQITQVGYFDECLRKYGNANWKYFTDLFDYLPALTALIEHIFCLHGLSPSLDTLDHI	177
Db	128	ASINRIYGYDECKERY-NIKLWKTFDFCNCLPIAAIVDEKIFCCHGSLSPDLQSQMEQI	186
Qy	178	RALDRIQEVPHEGPMCDLLWSDPD-DRCGWGISPRGAGYTFGQDIAEOPNHTNGLSLVAR	236
Db	187	RRIMRPTDVPDQGLLCDLLWSDPDKDVLGWGENDRGVSFTFGAEVVAKFLHKHDLDLICR	246
Qy	237	AHQLVMEGYNWCQDKNVVTVFSAPNYCYRCGNMAIMEIDETMNRSLQFEPAPROSEPD	296
Db	247	AHQVVEDGYEFFAKQQLVTLFSAPNYCGEFDNAGNMSVDETLMCSFQILPAEKK-KPN	305
Qy	297	VTRK-TP 302	
Db	306	ATRPVTP 312	

Search completed: December 9, 2005, 10:25:06
Job time : 47 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2005, 10:18:01 ; Search time 119 Seconds
(without alignments)
1074.418 Million cell updates/sec

Title: US-10-764-259-13
Perfect score: 1670
Sequence: 1 MPSYADVDRQIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1670	100.0	306	3	US-09-828-302-13
2	1670	100.0	306	4	US-10-764-259-13
3	1549	92.8	306	4	US-10-236-699-22
4	1547	92.6	306	4	US-10-236-699-32
5	1521	91.1	306	4	US-10-236-699-8
6	1521	91.1	306	4	US-10-425-115-345205
7	1518	90.9	312	4	US-10-425-114-72606
8	1508.5	90.3	307	4	US-10-236-699-26
9	1508.5	90.3	307	4	US-10-437-963-143206
10	1497.5	89.7	307	4	US-10-424-599-163708
11	1486	89.0	304	5	US-10-739-930-6733
12	1483	88.8	308	4	US-10-425-115-333776
13	1470	88.0	388	4	US-10-425-115-345209
14	1454	87.1	396	4	US-10-425-115-333773
15	1427	85.4	309	4	US-10-060-065-24
16	1427	85.4	309	4	US-10-060-065-39
17	1427	85.4	309	4	US-10-059-585-45
18	1427	85.4	309	4	US-10-059-585-60
19	1427	85.4	309	5	US-10-386-971-3
20	1408	84.3	314	4	US-10-236-699-24
21	1404	84.1	311	4	US-10-236-699-3
22	1392	83.4	313	4	US-10-311-764-5
23	1392	83.4	395	4	US-10-425-115-206998
24	1389	83.2	313	4	US-10-425-115-206995
25	1388	83.1	313	6	US-11-097-143-15735
26	1388	83.1	318	4	US-10-369-493-6189
27	1385	82.9	376	4	US-10-425-114-63887

28	1382	82.8	313	4	US-10-236-699-18	Sequ
29	1381	82.7	307	4	US-10-425-115-287936	Sequ
30	1379	82.5	307	4	US-10-236-699-30	Sequ
31	1378	82.5	307	4	US-10-425-115-287051	Sequ
32	1378	82.5	327	4	US-10-425-114-56755	Sequ
33	1378	82.5	374	4	US-10-425-114-40943	Sequ
34	1375	82.3	349	4	US-10-425-115-223093	Sequ
35	1373	82.2	311	4	US-10-424-599-166855	Sequ
36	1371.5	82.1	367	4	US-10-437-963-174105	Sequ
37	1368	81.9	307	4	US-10-437-963-103935	Sequ
38	1366	81.8	314	4	US-10-424-599-191175	Sequ
39	1337.5	80.1	304	5	US-10-739-930-10910	Sequ
40	1309.5	78.4	381	4	US-10-767-701-46140	Sequ
41	1308.5	78.4	419	4	US-10-369-493-2498	Sequ
42	1291	77.3	377	3	US-09-801-368-270	Sequ
43	1291	77.3	377	4	US-10-369-493-1551	Sequ
44	1286	77.0	369	3	US-09-801-368-268	Sequ
45	1286	77.0	369	4	US-10-369-493-1568	Sequ

ALIGNMENTS

RESULT 1
US-09-828-302-13
; Sequence 13, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 13
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-302-13

Query Match	100.0%	Score 1670;	DB 3;	Length 30
Best Local Similarity	100.0%	Pred. No. 7.9e-166;		
Matches 306;	Conservative 0;	Mismatches 0;	Indels	
QY	1	MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKCPVT		PH 60
DB	1	MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKCPVT		PH 60
QY	61	DLIELFRIGGKAPDNTYLFMGDYVDRGYVSVETVSLVALKVRDRIT		QI 120
DB	61	DLIELFRIGGKAPDNTYLFMGDYVDRGYVSVETVSLVALKVRDRIT		QI 120
QY	121	TQVYGFYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIFCLHGLSPS		AL 180
DB	121	TQVYGFYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIFCLHGLSPS		AL 180
QY	181	DRIEVPHGPMCDLLMSDDPDRCGWISPRGAGYTFQDIAEQFNHTG		QL 240
DB	181	DRIEVPHGPMCDLLMSDDPDRCGWISPRGAGYTFQDIAEQFNHTG		QL 240
QY	241	VMEGYNQCDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAE		RK 300
DB	241	VMEGYNQCDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAE		RK 300
QY	301	TPDYFL 306		

Db 301 TPDYFL 306

RESULT 2

US-10-764-259-13

; Sequence 13, Application US/10764259

; Publication No. US20040148658A1

GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE

; TITLE OF INVENTION: IN PLANTS

; FILE REFERENCE: 16313-0161

; CURRENT APPLICATION NUMBER: US/10/764,259

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Physcomitrella patens

US-10-764-259-13

Query Match 100.0%; Score 1670; DB 4; Length 306;

Best Local Similarity 100.0%; Pred. No. 7.9e-166;

Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPTVCGDIHGQFH 60

Db 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPTVCGDIHGQFH 60

Qy 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

Db 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

Qy 121 TVQYGFYDECLRKYGNNVWKFYTDLPYLPITALIEHIFCLHGLSPSLDTLDHIRAL 180

Db 121 TVQYGFYDECLRKYGNNVWKFYTDLPYLPITALIEHIFCLHGLSPSLDTLDHIRAL 180

Qy 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQNFHTNG: 240

Db 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQNFHTNG: 240

Qy 241 VMEGYNWCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAP: 300

Db 241 VMEGYNWCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAP: 300

Qy 301 TPDYFL 306

Db 301 TPDYFL 306

RESULT 3

US-10-236-699-22

; Sequence 22, Application US/10236699

; Publication No. US20030150028A1

GENERAL INFORMATION:

; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: COSTA E SILVA, OSWALDO DA

; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND

; TITLE OF INVENTION: METHODS OF USE IN PLANTS

; FILE REFERENCE: 16313-0161

; CURRENT APPLICATION NUMBER: US/10/236,699

; CURRENT FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: 60/317,305

; PRIOR FILING DATE: 2001-09-05

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Glycine max

US-10-236-699-22

Query Match 92.8%; Score 1549; DB 4; Length 306

Best Local Similarity 91.5%; Pred. No. 3.7e-153;

Matches 280; Conservative 16; Mismatches 10; Indels

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKCPVT 60

Db 1 MPSHADLERQIEQLMDCKPLSESEVKALCDQARTILVEEWNVQPKCPVT 60

Qy 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

Db 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

Qy 121 TVQYGFYDECLRKYGNNVWKFYTDLPYLPITALIEHIFCLHGLSPS: 180

Db 121 TVQYGFYDECLRKYGNNVWKFYTDLPYLPITALIEHIFCLHGLSPS: 180

Qy 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQNFHTNG: 240

Db 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQNFHTNG: 240

Qy 241 VMEGYNWCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAP: 300

Db 241 VMEGYNWCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAP: 300

Qy 301 TPDYFL 306

Db 301 TPDYFL 306

RESULT 4

US-10-236-699-32

; Sequence 32, Application US/10236699

; Publication No. US20030150028A1

GENERAL INFORMATION:

; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: COSTA E SILVA, OSWALDO DA

; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE:

; TITLE OF INVENTION: METHODS OF USE IN PLANTS

; FILE REFERENCE: 16313-0161

; CURRENT APPLICATION NUMBER: US/10/236,699

; CURRENT FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: 60/317,305

; PRIOR FILING DATE: 2001-09-05

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-236-699-32

Query Match 92.6%; Score 1547; DB 4; Length 306

Best Local Similarity 91.5%; Pred. No. 6e-153;

Matches 280; Conservative 15; Mismatches 11; Indels

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKCPVT 60

Db 1 MPSHADLERQIEQLMDCKPLSESEVKALCDQARTILVEEWNVQPKCPVT 60

Qy 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

Db 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALVKVRYDRITII 120

QY 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSPSLDTHIRAL 180
 DB 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSPSLDTHIRAL 180
 QY 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNGSLVARAHL 240
 DB 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNGSLVARAHL 240
 QY 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAPQSPDVTTRK 300
 DB 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAPQSPDVTTRK 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 5
 US-10-236-699-8
 ; Sequence 8, Application US/10236699
 ; Publication No. US20030150028A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOHNER, HANS J.
 ; APPLICANT: CHEN, RUOYING
 ; APPLICANT: ISHITANI, MANABU
 ; APPLICANT: VAN THIELEN, NOCHA
 ; APPLICANT: COSTA E SILVA, OSWALDO DA
 ; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
 ; TITLE OF INVENTION: METHODS OF USE IN PLANTS
 ; FILE REFERENCE: 16313-0161
 ; CURRENT APPLICATION NUMBER: US/10/236.699
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: 60/317,305
 ; PRIOR FILING DATE: 2001-09-05
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 US-10-236-699-8

Query Match 91.1%; Score 1521; DB 4; Length 306;
 Best Local Similarity 88.9%; Pred. No. 3.1e-150;
 Matches 272; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPSYADVDRQIEQLSECKPLSELEVNKLCDOARTILVEENVPVKCPVT 60
 DB 1 MPETGDIRQIEQLSECKPLSELEVNKLCDOARTILVEENVPVKCPVT 60
 QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120
 DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120
 QY 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSPSLDTHIRAL 180
 DB 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSPSLDTHIRAL 180
 QY 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNGSLVARAHL 240
 DB 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNGSLVARAHL 240
 QY 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAPQSPDVTTRK 300
 DB 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAPQSPDVTTRK 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 6

US-10-425-115-345205
 ; Sequence 345205, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425.115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 345205
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_77994C.1.pap
 US-10-425-115-345205

Query Match 91.1%; Score 1521; DB 4; Length 306
 Best Local Similarity 88.9%; Pred. No. 3.1e-150;
 Matches 272; Conservative 23; Mismatches 11; Indels 0;
 QY 1 MPSYADVDRQIEQLSECKPLSELEVNKLCDOARTILVEENVPVKCPVT 60
 DB 1 MPHADLDRLQSLRQDCKFLPEAEVKTLCEQAKALLMEENVPVKCPVT 60
 QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120
 DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120
 QY 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSP 180
 DB 121 TQVGYFDECLRKYGNNVWKFYDLDYPLTALIEHIEFCLHGGSLSP 180
 QY 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNG 240
 DB 181 DRIQVPEHGMCDLLWSDPDRCGWISPRGAGYTFQGDIAEQNHTNG 240
 QY 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAP 300
 DB 241 VMEGYNWQDKNVTVFSAFNVCYRCGNMAALMEIDETMNSFLQFEPAP 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 7
 US-10-425-114-72606
 ; Sequence 72606, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improv
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425.114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72606
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mexicana
 ; FEATURE:

ated With

Db . 121 ITQVGYDECLRKYGNAVWKFYTDLFDYLP LPTALIQVFC LHGGLSPSLDLDNIRA 180

; Sequence 163708, Application US/104224599
; Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163708
LENGTH: 307
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(307)
OTHER INFORMATION: unsure at all Xaa locations
OTHER INFORMATION: Clone ID: PAT_MRT3847_118848C.1.pep
US-10-424-599-163708

Query Match 89.7%; Score 1497.5; DB 4; Length 307;
Best Local Similarity 88.6%; Pred. No. 9.1e-148;
Matches 272; Conservative 16; Mismatches 18; Indels 1; Gaps 1;
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVTTCGDIHGQPH 60
DB 1 MPSHADLSEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVTTCGDIHGQFY 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILRGHNSRQI 120
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILXGNHESRQI 120
QY 121 TQVGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPSLDLHDHRA 179
DB 121 TQVGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPSLDLDNIRA 180
QY 180 LDRIQEVPHGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSVARHQ 239
DB 181 LDRIQEVPHGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLISRAHQ 240
QY 240 LVMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSRFLQEPAPRQSEPDVTR 299
DB 241 LVMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSRFLQEPAPRQSEPDVTR 300
QY 300 KTPDYFL 306
DB 301 KTPDYFL 307

RESULT 11
US-10-739-930-6733
Sequence 6733, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 6733
LENGTH: 304
TYPE: PRT
ORGANISM: Arabidopsis thaliana
NAME/KEY: unsure
LOCATION: (1)..(304)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:

OTHER INFORMATION: Clone ID: ARATH-23APR03-C8015_1.p
US-10-739-930-6733
Query Match 89.0%; Score 1486; DB 5; Length 304
Best Local Similarity 88.2%; Pred. No. 1.4e-146;
Matches 270; Conservative 16; Mismatches 18; Indels
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
DB 1 MPSNGDLDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
QY 121 TQVGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPS
DB 121 T--XGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPS
QY 181 LDRIQEVPHGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGL
DB 179 LDRIQEVPHGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGL
QY 241 LVMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSRFLQEPAPR
DB 239 LVMEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNSRFLQEPAPR
QY 301 TPDYFL 306
DB 299 TPDYFL 304

RESULT 12
US-10-425-115-333776
Sequence 333776, Application US/104251115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333776
LENGTH: 308
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(308)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_67515C.1.pep
US-10-425-115-333776

Query Match 88.8%; Score 1483; DB 4; Length 308
Best Local Similarity 87.0%; Pred. No. 3e-146;
Matches 268; Conservative 24; Mismatches 14; Indels
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
DB 1 MPSHGDLDRQIAQLRDKYLPKAEVKNLDCQARTILVEEWNVPVKCPVT
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
QY 121 TQVGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPS
DB 121 TQVGYFDECLRKYGNNVWKYFTDLFDYPLTALIEHIEIFCLHGGSPS

ated With

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Db 121 TQVGYFDECLRYKGNANWKYFTDLFDLPLTALLENQVFLHGLSPSLDLDNIRSL 180
Qy 181 DRIQEVF-HEGPMCDLLWSDDPDRCGWISPRGAGYTFQDIAEONHTNGLSLVARAHQ 239
Db 181 DRVQEVPHGPMCDLLWSDDPDRCGWISPRGAGYTFQDIAEONHTNGLSLVARAHQ 240
Qy 240 LVMEGYNWCDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPR-QSEPDVT 298
Db 241 LVMEGYNWCDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPR-QSEPDVT 300
Qy 299 RKTPDYFL 306
Db 301 RKTPDYFL 308

RESULT 13
US-10-425-115-345209
; Sequence 345209, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345209
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(388)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_77998C.1.pap
US-10-425-115-345209
Query Match 88.0%; Score 1470; DB 4; Length 388;
Best Local Similarity 70.1%; Pred. No. 9.6e-145;
Matches 272; Conservative 23; Mismatches 11; Indels 82; Gaps 1;

Qy 1 MPSYADVDRQIEQLSECKPLSEVLNLCDOARTILVEENWVQPKVPCVTGDIHQFH 60
Db 1 MPHADLDLDRQISQLRDKFLPEAEVKTICEQAKALMBEENWVQVRCPTVCGDIHQFY 60
Qy 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLKVRDRITILRGNHESRQI 120
Db 61 DLIELFRIGGAPDNTNLYFMGDYVDRGYYSVETVSLVALLKVRDRITILRGNHESRQI 120
Qy 121 TQV----- 123
Db 121 TQVGYFDECLRYKGNANWKYFTDLXLFDVPRWKNFLDYCRFCGXDRIXIPNQLQIT 180
Qy 124 -----YGFYDECLRYKGNANWKYFTDLFDLPLTALIEH 158
Db 181 WSGFLTVGHYSACLGLNPXTPTRYGFYDECLRYKGNANWKYFTDLFDLPLTALLEN 240
Qy 159 EIFCLHGLSPSLDLDLHIALDRIOEVPHGPMCDLLWSDDPDRCGWISPRGAGYTFG 218
Db 241 QIFCLHGLSPSLDLDLHIALDRIOEVPHGPMCDLLWSDDPDRCGWISPRGAGYTFG 300
Qy 219 ODIAEQFNHTNGLSLVARAHQLVMEGYNWCDKNVTVFSAPNYCYRCGNMAAIMEIDET 278
Db 301 QDIAEQFNHTNGLSLVARAHQLVMEGYNWCDKNVTVFSAPNYCYRCGNMAAIMEIDEN 360
Qy 279 MNRSFLOFEPAPRQSEPDVTRKTPDYFL 306
Db 361 MDQNFLOFDPAPRQIEPDVTRKTPDYFL 388
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RESULT 14

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US-10-425-115-333773
; Sequence 333773, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 333773
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(396)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_67512C.1.pap
US-10-425-115-333773
Query Match 87.1%; Score 1454; DB 4; Length 396
Best Local Similarity 67.9%; Pred. No. 4.7e-143;
Matches 269; Conservative 24; Mismatches 13; Indels 3;

Qy 1 MPSYADVDRQIEQLSECKPLSEVLNLCDOARTILVEENWVQPKVPCVT 60
Db 1 MPBGDLDRQIAQLRDKCYLPEAEVKALCEQAKALMBEENWVQVRCPTV 60
Qy 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLKVRDRITIL 120
Db 61 DLIELFRIGGAPDNTNLYFMGDYVDRGYYSVETVSLVALLKVRDRITIL 120
Qy 121 TQVGYFDECLRYKGNANWKYFTDLFDLPLTALIEHIEIFCLHGLSPS: 180
Db 121 TQVGYFDECLRYKGNANWKYFTDLFDLPLTALIEHIEIFCLHGLSPS: 180
Qy 181 DRIQ----- 184
Db 181 DRVQEVFIRAMSGNCRILPNKXSIQIDMFNP IQKLDNIEIIRQPYKNDV 240
Qy 185 -----EVPHEGPMCDLLWSDP 210
Db 241 VFFSHSFFLLGWGVSLRLDISPLVKQPVVICNEVPHEGPMCDLLWSDP 300
Qy 211 RGAGYTFQDIAEQFNHTNGLSLVARAHQLVMEGYNWCDKNVTVFSAP 270
Db 301 RGAGYTFQDIAEQFNHTNGLSLVARAHQLVMEGYNWCDKNVTVFSAP 360
Qy 271 AIMEIDETMNRSELOFEPAPRQSEPDVTRKTPDYFL 306
Db 361 AILBEIGNMNQFLQFDPAFPRIEPTDTRKTPDYFL 396

RESULT 15
US-10-060-065-24
; Sequence 24, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayaashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
```


APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Keiichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Jun-ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-065-24

Query Match 85.4%; Score 1427; DB 4; Length 309;
Best Local Similarity 83.7%; Pred. No. 2.2e-140;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

Qy	6	DVDRQIEQLSECKPLSELEVNLCDOARTILVEENWVQPKCPVTCGDIHQPHDLIEL	65
Db	9	ELDQWIEQLNECKQLSESKLCEKAEIITKESNVQEVRCPTVCGDVHGQFHDLMEL	68
Qy	66	FRIGGKAPDTNLYLFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGNHESRQITQVYG	125
Db	69	FRIGGKSPDTNLYLFMGDYVDRGYYSVETVLLVALKVRYRERITILRGNHESRQITQVYG	128
Qy	126	FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRALDRIOE	185
Db	129	FYDECLRKYGNANWKYFTDLFDYLPALTALVDGQIFCLHGLSPSIDTLDIRALDRIOE	188
Qy	186	VPHGPMCDLLWSDDRCGWGISPRGAGYTFGODIAEQENHTNGLSLAVARAHQLVMEGY	245
Db	189	VPHGPMCDLLWSDDRCGWGISPRGAGYTFGQDISETFNLANGTLVSRAHQLVMEGY	248
Qy	246	NWCODKNVTVFSAFNPCYRCGNMAAIMEIDETWNRSFLQEPAPRQSEPDVTRKTPDYF	305
Db	249	NWCHDRNVTVFSAFNPCYRCGNQAAINELDDTLKYSFLQFPAPRGPVTRTPDYF	308
Qy	306	L 306	
Db	309	L 309	

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Job time : 120 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:20:31 ; Search time 38 Seconds
(without alignments)
44.969 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1427	85.4	309	7 US-11-109-156-24	Sequence 24, Appl
2	1427	85.4	309	7 US-11-109-156-39	Sequence 39, Appl
3	757	45.3	319	7 US-11-109-156-38	Sequence 38, Appl
4	757	45.3	323	6 US-10-878-556A-184	Sequence 184, Appl
5	757	45.3	323	7 US-11-109-156-37	Sequence 37, Appl
6	565	33.8	521	7 US-11-109-156-34	Sequence 34, Appl
7	87.5	5.2	276	6 US-10-467-657-2502	Sequence 2502, Ap
8	87	5.2	250	7 US-11-135-855-41	Sequence 41, Appl
9	76.5	4.6	316	6 US-10-485-517-370	Sequence 370, Appl
10	76.5	4.6	696	7 US-11-029-003-8	Sequence 8, Appl
11	76	4.6	264	6 US-10-467-657-6940	Sequence 6940, Ap
12	75.5	4.5	677	7 US-11-058-727-52	Sequence 52, Appl
13	75.5	4.5	677	7 US-11-058-727-84	Sequence 84, Appl
14	75.5	4.5	677	7 US-11-108-389-52	Sequence 52, Appl
15	75.5	4.5	677	7 US-11-108-389-84	Sequence 84, Appl
16	74.5	4.5	459	6 US-10-793-626-1246	Sequence 1246, Ap
17	74.5	4.5	459	6 US-10-793-626-2554	Sequence 2554, Ap
18	74	4.4	518	6 US-10-793-626-2554	Sequence 506, Appl
19	72.5	4.3	267	7 US-10-495-597-5	Sequence 5, Appl
20	72.5	4.3	673	7 US-11-058-727-14	Sequence 14, Appl
21	72.5	4.3	673	7 US-11-108-389-14	Sequence 14, Appl
22	72.5	4.3	1210	7 US-11-058-727-4	Sequence 4, Appl
23	72.5	4.3	1210	7 US-11-108-389-4	Sequence 4, Appl
24	72	4.3	406	6 US-10-770-726-73	Sequence 73, Appl
25	71.5	4.3	472	6 US-10-689-742-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-11-109-156-24
; Sequence 24, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTE

TITLE OF INVENTION: PHOSPHATASE

FILE REFERENCE: 06501-099002

CURRENT APPLICATION NUMBER: US/11109,156

PRIOR FILING DATE: 2005-04-19

PRIOR APPLICATION NUMBER: US/10/060,065

PRIOR FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05061

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: JP 11-248036

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 24

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

US-11-109-156-24

Qy	118	ROITQVGYGYSCLARKYGNANVWKYFTDLPYLPPLTALIEHETPCLHGGSLSPSLDLTHI	177
Db	128	ASINRIYGYDECKERY-NIKLWKTFTDFCNCLPTAAIVDEKIFCCCHGGLSPDLQSMEQI	186
Qy	178	RALDRLOEYVPHGPGWCDLLWSDDP-DRCGWGISPRGAGYTFGQDIAEQFNHTNGLSIVAR	236
Db	187	RRIMRPTDVPDQGLCDLLWSDDPKDVLGWGENDRGVSFTFGAEVWAKFVLKHKHDLOLI	246
Qy	237	AHOLVMGYNWCQDKNNVTVFSAPNYCYRCNGMAAIMEIDETMNRSLQEPAPROSEPD	296
Db	247	AHQVVEDGVEYFAKRLQVLTLFSAPNYCGEFDNAGAMMSVDETLMCSFOILKPAEKK-KPN	305
Qy	297	VTRK-Tp 302	
Db	306	ATSPVTP 312	

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RESULT 6
US-11-109-156-34
; Sequence 34, Application US/1109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-34

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[illegible]

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RESULT 7
US-10-467-657-2502
; Sequence 2502, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2502
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2502

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RESULT 8
US-11-135-855-41
: Sequence 41, Application US/11135855
: Publication No. US2005025557A1
: GENERAL INFORMATION:
: APPLICANT: SMITHKLINE BEECHAM CORPORATION
: APPLICANT: SMITHKLINE BEECHAM P.L.C.
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP50013
: CURRENT APPLICATION NUMBER: US/11/135,855

[illegible]

QY 269 MAAMEIDETMRSFLQEPAPRQSEPDVTRKTP 302
Db 575 KALPAPIERTISKA----KGQPR--EPQVYTLPP 602

RESULT 11

US-10-467-657-6940
; Sequence 6940, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6940
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6940

Query Match 4.6%; Score 76; DB 6; Length 264;
Best Local Similarity 22.5%; Pred. No. 1.7;
Matches 36; Conservative 18; Mismatches 60; Indels 46; Gaps 8;
QY 125 GFDVDECLRKRYGNANWKYPTDLFDY-----LPLTALIEHEIFCLHGLGSLSPSLDTLDHI 177
Db 65 GMLSALLQKQISANTW-LFNDLCDVRSRLAEKLPS-----PFDYCDENFFPQFQFDLI 119
QY 178 RALDRIQEVHPGPMCDLLWSDD-----RCWGGISPRG--AGYTFGQDIAEQFNHTGL 231
Db 120 ASASAVQ-----WFHPQDAFIAHCKTGLKTNGLLAVATFGKDNLKEVRQITNI 167
QY 232 SL-----VARAHLVMEGYNWCDKNVTVFSAP 260
Db 168 GLNYPTLSQWAWLAKDFELL-----WCEDFKVILDFDTP 202

RESULT 12

US-11-058-727-52
; Sequence 52, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-52

Query Match 4.5%; Score 75.5; DB 7; Length 677
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 1.
QY 7 VDRQIEQLSECKPLSELEVNKLCDQARTILVEENNVQVKCPVTVCG---
Db 123 INQIAEYARNKALSELEGLGNYYQLYLTALEEWENPFRRSGSLNGSRP;
QY 61 DLIELF-----RIGGKAPDTNYLFMGD---YVDRGYYS'
Db 193 ILDSLFTQYMPSFRVTNPEVFLTVYAMAANLHLLLLKXDAIFGEWGS'
QY 101 KRYRDRITILRGNHESRQITQVYGFVDECURKY-----GNANVWK
Db 238 -----NYDRQMKLTAEYSDHCVKVETGLAKLGTSAKQWV'
QY 152 LTALIEHEIFCLHGLGSLSPSLDTLDHIRALDRIQEVHPGPMCDLLWSDDP;
Db 285 LAVLDVVALF-----PNYDT-----RTYMETKAQLTREVITDPL
QY 212 GAGY-----TFQGDIAEQ-----FNHTNGLSLVARA-----
Db 328 GSWYDKAPSGF--VIESSVIRPPHVDYITGLTVYTQSRSSSARYIRHW
QY 241 -----VMEGYNWCQKNVTVFSAPNY-CYRCGNMAAIM-----
Db 386 SRGSLNQMYGTQNQLHSTSTFDFTNDYIKTSLKDAVLLDIVYEGYTYI:
QY 279 M-----NRSFLQEP-----APROSE---PDVTRKTPDY 304
Db 446 MVNQLNTRKTLKYNPVSOKIILASTRSELELPETSDQPNY 487

RESULT 13

US-11-058-727-84
; Sequence 84, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-84

Query Match 4.5%; Score 75.5; DB 7; Length 677;
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;
QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG-----DTHGQFH 60
DB 123 INQKIAEYARNKALSEGLEGNNGYQLYLTALBEWENPFRRSGSLNGSRPALRDVNRNFE 182
QY 61 DLIELF-----RIGGKAPDNTNLYFMGD---YVDRGYYSVETVSLVAL 100
DB 183 ILDSLFTQMPSPRVNTNEVFLTVYAMAANLHLLLLKADASIFGEWGSVTTIN----- 237
QY 101 KVRVDRITILRGHNSHQITQVGYFDECLRY-----GNANVWKYFTDLFDYLP 151
DB 238 -----NYDROMKLTAEYSDHCVKWYETGLAKGTSAKQWVDVYQPRREMT 284
QY 152 LTALIEHETFCLHGLSPSLDTLDIRALDRIOEVPHEGPMCDLLWSDDRCGHSIPR 211
DB 285 LAVLDVVALF-----PNYDT-----RYPMETKAQLTREYVTDPLGAV--NVSSI 327
QY 212 GAGY----TFGQDIAEQ-----FNHTNGLSLVARA-----HQL----- 240
DB 328 GSWYDKAPSGF--VLESSVIRPPHVDYITGLTVYTQSRSSARYIRHWAGHQSIRHV 385
QY 241 -----VMEGYNCQDNVTVFSAPNY-CYRCGNMAAIM-----EIDET 278
DB 386 SRGSLNQMYGTNQLHSTSTFDTNVDYIKTSLDKAVLLDIVPGYTVIFGMEVEFF 445
QY 279 M-----NRSELOFEP-----APROSE---PDVTRKTPDY 304
DB 446 MVNQLNTRKTLKYNPVSVDIIASTRDESELELPPEPSTQPNY 487

RESULT 14
US-11-108-389-52
; Sequence 52, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-52

Query Match 4.5%; Score 75.5; DB 7; Length 677;
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;
QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG-----DTHGQFH 60
DB 123 INQKIAEYARNKALSEGLEGNNGYQLYLTALBEWENPFRRSGSLNGSRPALRDVNRNFE 182

QY 61 DLIELF-----RIGGKAPDNTNLYFMGD---YVDRGYYS
DB 183 ILDSLFTQMPSPRVNTNEVFLTVYAMAANLHLLLLKADASIFGEWGS
QY 101 KVRVDRITILRGHNSHQITQVGYFDECLRY-----GNANVWK
DB 238 -----NYDROMKLTAEYSDHCVKWYETGLAKGTSAKQWV
QY 152 LTALIEHETFCLHGLSPSLDTLDIRALDRIOEVPHEGPMCDLLWSDDL
DB 285 LAVLDVVALF-----PNYDT-----RYPMETKAQLTREYVTDPL
QY 212 GAGY----TFGQDIAEQ-----FNHTNGLSLVARA-----
DB 328 GSWYDKAPSGF--VLESSVIRPPHVDYITGLTVYTQSRSSARYIRHW
QY 241 -----VMEGYNCQDNVTVFSAPNY-CYRCGNMAAIM-----
DB 386 SRGSLNQMYGTNQLHSTSTFDTNVDYIKTSLDKAVLLDIVPGYTVI
QY 279 M-----NRSELOFEP-----APROSE---PDVTRKTPDY 304
DB 446 MVNQLNTRKTLKYNPVSVDIIASTRDESELELPPEPSTQPNY 487

RESULT 15
US-11-108-389-84
; Sequence 84, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-108-389-84

Query Match 4.5%; Score 75.5; DB 7; Length 677
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;
QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG---
DB 123 INQKIAEYARNKALSEGLEGNNGYQLYLTALBEWENPFRRSGSLNGSR
QY 61 DLIELF-----RIGGKAPDNTNLYFMGD---YVDRGYYS
DB 183 ILDSLFTQMPSPRVNTNEVFLTVYAMAANLHLLLLKADASIFGEWGS
QY 101 KVRVDRITILRGHNSHQITQVGYFDECLRY-----GNANVWK
DB 123 INQKIAEYARNKALSEGLEGNNGYQLYLTALBEWENPFRRSGSLNGSRPALRDVNRNFE 182

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:23:27 ; Search time 561 Seconds
(without alignments)
3635.287 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgm2_1/USPRO_spool_p/US10764259/runat_05122005_094547_7008/app_query.fasta.1.455
-DB=N_Geneseq -OFT=fastp -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10764259 @CGN 1.1.1096 @runat_05122005_094547_7008 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	1365	6	ABN81332 Physcomit
2	1670	100.0	1365	8	ABX16239 P. patens
3	1549	92.8	1386	10	ACC43349 Protein p
4	1547	92.6	1330	10	ACC43354 Protein p

5	1522	91.1	921	3	AAC43084	Aac43
6	1521	91.1	1243	10	ACC43342	Acc4
7	1518	90.9	1732	13	ADX44434	Adx6
8	1514	90.7	1267	3	AAC40149	Aac40
9	1509	90.4	1422	3	AAC46572	Aac46
10	1508.5	90.3	1298	10	ACC43351	Aac4
11	1508	90.3	921	3	AAC43368	Aac43
12	1508	90.3	921	6	ABZ12900	Abz12
13	1504	90.1	1344	3	AAC44779	Aac44
14	1495	89.5	924	6	ABZ12766	Abz12
15	1495	89.5	1110	3	AAC42354	Aac42
16	1478.5	88.5	1259	3	AAC45630	Aac45
17	1452	86.9	1759	13	ADX50122	Adx5
18	1431	85.7	1626	13	ADX54215	Adx5
19	1429	85.6	1484	13	ADT15863	Adt1
20	1427	85.4	1738	11	ADW22195	Adw2
21	1427	85.4	1738	12	ADP72938	Adp7
22	1427	85.4	1787	3	AAZ36719	Aaz36
23	1427	85.4	1804	6	ABK63717	Abk63
24	1427	85.4	1804	10	ADB58231	Adb5
25	1427	85.4	1804	10	ADB52760	Adb5
26	1427	85.4	1804	13	ADV41052	Adv4
27	1427	85.4	1804	14	ADY97843	Ady9
28	1427	85.4	2181	6	ABV94193	Abv94
29	1427	85.4	2181	10	ADB85531	Adb8
30	1427	85.4	2181	10	ADC16746	Adc1
31	1427	85.4	2181	10	AAD51128	Aad5
32	1427	85.4	2181	12	ADL83147	Adl8
33	1427	85.4	2181	14	ADX05673	Adx0
34	1427	85.4	2181	14	ADZ11994	Adz1
35	1427	85.4	2966	6	ABK84047	Abk84
36	1411	84.5	930	6	AB199353	Ab199
37	1411	84.5	1522	12	ADQ85030	Adq8
38	1411	84.5	1531	10	ADD18470	Adl1
39	1411	84.5	1541	10	ADB85530	Adb8
40	1411	84.5	1541	10	ADC16745	Adc1
41	1411	84.5	1541	10	AAD51130	Aad5
42	1411	84.5	1541	14	ADX08186	Adx0
43	1411	84.5	1541	14	ADX03728	Adx0
44	1411	84.5	1580	11	ADW22196	Adw2
45	1411	84.5	1843	6	ABT07396	Abt07

ALIGNMENTS

RESULT 1

ABN81332

ID ABN81332 standard; cDNA; 1365 BP.

XX

AC ABN81332;

XX

DT 02-SEP-2002 (first entry)

XX

DE Physcomitrella patens PP2A-4 encoding cDNA SEQ ID NO 8.

XX

KW Physcomitrella patens; PHSRP; phosphatase stress related pr

KW PP2C; enzyme; transgenic; plant; stress tolerance; gene; ss

XX

OS Physcomitrella patens.

XX

FH Key Location/Qualifiers

FT CDS 71..991

FT /*tag= a

FT /product= "PP2A-4"

XX

FN WO200246442-A2.

XX

PD 13-JUN-2002.

XX

PF 06-APR-2001; 2001WO-US011253.

XX

PR 07-APR-2000; 2000US-0196001P.

XX

PP2A;

PA (BADI) BASF PLANT SCI GMBH.
XX Da Costa E SilvaO, Bohnert HJ, Ishitani M, Van Thielen N, Chan R;
XX WPI; 2002-508562/54.
DR P-PSDB; ABB77578.
XX New transgenic plant cell transformed by phosphatase stress-related
PT protein coding nucleic acid whose expression in the cell results in
PT increased tolerance to environmental stress compared to wild type cell.
XX Claim 18; Fig 2; 106pp; English.
XX The invention relates to a transgenic plant cell (I) transformed by a
CC phosphatase stress-related protein (PHSRP) coding nucleic acid (ABN81330-
CC ABN81334), where expression of the nucleic acid in the plant cell results
CC in increased tolerance to an environmental stress as compared to a wild
CC type variety of the plant cell. PHSRP encoding genes are useful for
CC identifying Physcomitrella patens and related organisms, as markers for
CC specific regions of the genome, mapping of genomes of organisms related
CC to P. patens, identification and localisation of P. patens sequences of
CC interest, evolutionary studies, determination of PHSRP regions required
CC for function, modulation of a PHSRP activity, modulation of the
CC metabolism of one or more cell functions, modulation of the transmembrane
CC transport of one or more compounds and modulation of stress resistance.
CC The gene is also useful for identifying and/or cloning PHSRP homologues
CC in other cell types and organisms, for identifying an organism as being
CC P. patens or its close relative and for evolutionary and protein
CC structural studies. The present sequence is that of a PHSRP encoding
CC polynucleotide of the invention
XX
SQ Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x ABN81332 (1-1365)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysLysProLeu 20
Db 71 ATGCGTGCATATGCAGATGTAGACCGGAGATAGACAGCTGTCGGAGTGCAGGCGTTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLutrp 40
Db 131 TCGGAGTTGGAGGTGAAGAACCTATGTATCAAGCTCGACGATCTTGGTGGAGGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 191 AACGTGCAGCCGTCGAAGTGTCTGTACGGTTCGCGGTGACATCATGGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrIleuPheMet 80
Db 251 GATCTCATCGAGCTTTTCGCGATAGGAGCGCAAGGCGCCCGACACCACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
Db 311 GCGGACTATGTGGATCGTGATATTTCTGTGAGACGTGTGCTCTTAGTGGCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 371 AAGGTGCGGTATAGGATAGGATCAATCTTTGCGAGGAAACACGAGAGCGAGATT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db 431 ACGCAAGTATATGGTTTCTATGATGAATGCTCGCGAAGATGGAATGCGAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160

Db 491 AAGTACTTCAGGATCTGTTGCGACTACTGCTGCTGACAGCTCTCATTCGA
QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIle
Db 551 TTTTGTCTTCATGCTGGTCTGCTCTCCATCGCTCGACACATTAGATCAT
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp
Db 611 GATCGTATTCAGAAGTGCACGAGGCGCCGATGTGTGATCTACTCTG
QY 201 AspAspArgCysGlyTyrGlyLysSerProArgGlyAlaGlyTyrThrPhe
Db 671 GATGATCGTTGTGATGGGCAATTTTCCACGAGGTCGGGTATACTTT
QY 221 IleAlaGluInPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla
Db 731 ATTGCAGAGCAGTTCATCATACCAATGGTCTAAGTTTGGTTGCACGTGC
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhe
Db 791 GTGATGGAAGGATACAATTGGTGCAGGATAAAATGTTGTCCACAGTTT
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly
Db 851 AATTACTGTTACCGCTGTGGAAACATGCGCCCATATGGAGATAGATGA
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal
Db 911 CGGTCTTTTCTCAGTTTCGAACACGACCGCGGCAAGTGAACCAAGATGT
QY 301 ThrProAspTyrPheLeu 306
Db 971 ACTCTGATTACTTTCTG 988

RESULT 2
ABX16239
ID ABX16239 standard; cDNA; 1365 BP.
XX AC ABX16239;
XX DT 08-APR-2003 (first entry)
XX DE P. patens protein phosphatase PP2A-4 cDNA.
XX KW Plant; ss; gene; PP2A-4; protein phosphatase; PHSRP; cold; i
KW phosphatase stress related protein; environmental stress; d
KW salt tolerance.
XX OS Physcomitrella patens.
XX FH Key Location/Qualifiers
FT CDS 71..991
FT /*tag= a
FT /product= "PP2A-4"
XX US2002152502-A1.
XX PD 17-OCT-2002.
XX PF 06-APR-2001; 2001US-00828302.
XX PR 07-APR-2000; 2000US-0196001P.
XX (SILV/) DA COSTA E SILVA O.
PA (BOHN/) BOHNERT H J.
PA (VTHI/) VAN THIELEN N.
PA (CHEN/) CHEN R.
PA (ISHI/) ISHITANI M.
XX Da Costa E SilvaO, Bohnert HJ, Van Thielen N, Chan R, I
XX WPI; 2003-198392/19.
XX P-PSDB; ABB74203.

XX New transgenic plant cell transformed by a Phosphatase Stress-Related
 PT Protein (PHSRP) coding nucleic acid, useful for modifying stress
 PT tolerance of a plant.
 XX
 PS Claim 18; Fig 2C; 79pp; English.
 XX
 CC The invention relates to a transgenic plant cell transformed by a
 CC Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid. The
 CC expression of the nucleic acid in the plant cell results in increased
 CC tolerance to an environmental stress (e.g. salt tolerance, cold and
 CC drought) as compared to a wild type variety of the plant cell. Also
 CC include are a transgenic plant comprising the novel plant cell, a seed
 CC produced by the transgenic plant of (where the seed is true breeding for
 CC an increased tolerance to environmental stress as compared to a wild type
 CC variety of the plant cell, an agricultural product produced by the plant
 CC or seed, an isolated PHSRP or PHSRP coding nucleic acid, a recombinant
 CC expression vector comprising the nucleic acid, and producing a transgenic
 CC plant containing PHSRP nucleic acid. The transgenic plant cell
 CC transformed by a Phosphatase Stress-Related Protein (PHSRP) coding
 CC nucleic acid is useful for modifying stress tolerance of a plant. The
 CC present sequence encodes the PHSRP, protein phosphatase, PP2A-4
 XX
 SQ Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9,72e-180 Length: 1365
 Score: 1670.00 Matches: 306
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-764-259-13 (1-306) x ABX16239 (1-1365)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
 DB 71 ATGCGTGCATATGAGATGATAGACGGCAGATAGACGAGCTGCGAGTGCAAGCGGTG 130
 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLysTrp 40
 DB 131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGAGACGATCTTGGTGAGAGTGG 190
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
 DB 191 AACGTGACGCGGTGAGTGTCTCTACGGTTTGGGTGACATCCATGGCCAGTTTCAT 250
 QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrIleuPheMet 80
 DB 251 GATCTCATCGAGCTTTCCGCATAGGAGCAAGGCGCCGACACCACTACTTGTTCATG 310
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 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa YS 300
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 DT 11-AUG-2003 (first entry)
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 KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
 KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
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 OS Glycine max.
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 FT CDS 92..1012
 FT /*tag= a
 FT /product= "protein phosphatase stress-relat
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 PD 13-MAR-2003.
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 PF 05-SEP-2002; 2002WO-US028445.
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 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Bohnert HU, Chen R, Ishitani M, Van Thielien N, Da Costa O;
 XX WPI; 2003-300886/29.
 DR P-PSDB; ABP98034.
 XX
 PT New protein phosphatase stress-related polypeptide coding n
 PT useful for modulating plant's tolerance to an environmental
 PT as drought, increased salinity and cold.
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 PS Claim 1; Page 82; 107pp; English.
 CC The present sequence encodes a protein phosphatase stress-r
 CC polypeptide (PPSRP). The specification describes PPSRP poly
 CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3,

CC GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from
CC Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
CC polypeptides and polynucleotides are useful for modulating plant
CC tolerance to an environmental stress such as drought or increased
CC salinity and cold. They are also useful in identification and
CC localization of Physcomitrella patens, Brassica napus, Glycine max or
CC Oryza sativa and related organisms, mapping of genomes of organisms
CC related to the above species, in a evolutionary and polypeptide
CC structural studies, in determination of PPSRP regions required for
CC function, modulation of PPSRP activity, modulation of metabolism of one
CC or more cell functions and transmembrane transport of one or more
CC components
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AC ACC43354;
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DT 11-AUG-2003 (first entry)
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KW Protein phosphatase stress-related polypeptide; PPSRP; PpPP;
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;)
KW drought; salinity; cold; enzyme; gene; ss.
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OS Oryza sativa.
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FH Key Location/Qualifiers
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FT polypeptide"
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PD 13-MAR-2003.
XX
PP 05-SEP-2002; 2002WO-US028445.
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PR 05-SEP-2001; 2001US-0317305P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa
XX
DR WPI; 2003-300886/29.
XX
DR P-PSDB; ABP98039.
XX
PT New protein phosphatase stress-related polypeptide coding m
PT useful for modulating plant's tolerance to an environmental
PT as drought, increased salinity and cold.
XX
PS Claim 1; Page 87-88; 107pp; English.
XX
CC The present sequence encodes a protein phosphatase stress-r
CC polypeptide (PPSRP). The specification describes PPSRP poly
CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, (
CC GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
CC Physcomitrella patens, Brassica napus, Glycine max or Oryza
CC polypeptides and polynucleotides are useful for modulating
CC tolerance to an environmental stress such as drought or inc
CC salinity and cold. They are also useful in identification an
CC localization of Physcomitrella patens, Brassica napus, Glyc
CC Oryza sativa and related organisms, mapping of genomes of o
CC related to the above species, in a evolutionary and polypep
CC structural studies, in determination of PPSRP regions requi
CC function, modulation of PPSRP activity, modulation of metab

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AC ACC43342;
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DT 11-AUG-2003 (first entry)
XX
DE Protein phosphatase stress-related polypeptide BnPP2A-1 cDNA.
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XX New protein phosphatase stress-related polypeptide coding n
XX useful for modulating plant's tolerance to an environmental
XX as drought, increased salinity and cold.
XX
XX Claim 1; Page 74-75; 107pp; English.
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XX The present sequence encodes a protein phosphatase stress-r
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XX Physcomitrella patens, Brassica napus, Glycine max or Oryza
XX polypeptides and polynucleotides are useful for modulating
XX tolerance to an environmental stress such as drought or inc
XX salinity and cold. They are also useful in identification a
XX localization of Physcomitrella patens, Brassica napus, Glyc
XX Oryza sativa and related organisms, mapping of genomes of c
XX related to the above species, in a evolutionary and polypef
XX structural studies, in determination of PPSRP regions requi
XX function, modulation of PPSRP activity, modulation of metabol
XX or more cell functions and transmembrane transport of one c
XX components
XX
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Db 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln
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Protein phosphatase stress-related polypeptide; PPSRP; PpPf
BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
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drought; salinity; cold; enzyme; gene; ss.
Brassica napus.

Key Location/Qualifiers
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13-MAR-2003.

05-SEP-2002; 2002WO-US028445.

05-SEP-2001; 2001US-0317305P.

(BADI) BASF PLANT SCI GMBH.

Bohnert HU, Chen R, Ishitani M, Van Thielén N, Da Costa
WPI; 2003-300886/29.
P-PSDB; ABP98027.

New protein phosphatase stress-related polypeptide coding n
useful for modulating plant's tolerance to an environmental
as drought, increased salinity and cold.

Claim 1; Page 74-75; 107pp; English.

The present sequence encodes a protein phosphatase stress-r
polypeptide (PPSRP). The specification describes PPSRP poly
designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3,
GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
Physcomitrella patens, Brassica napus, Glycine max or Oryza
polypeptides and polynucleotides are useful for modulating
tolerance to an environmental stress such as drought or inc
salinity and cold. They are also useful in identification a
localization of Physcomitrella patens, Brassica napus, Glyc
Oryza sativa and related organisms, mapping of genomes of c
related to the above species, in a evolutionary and polypef
structural studies, in determination of PPSRP regions requi
function, modulation of PPSRP activity, modulation of metabol
or more cell functions and transmembrane transport of one c
components

Sequence 1243 BP; 337 A; 258 C; 299 G; 349 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.88e-163 Length: 1243
Score: 1521.00 Matches: 272
Percent Similarity: 95.42% Conservative: 20
Best Local Similarity: 88.89% Mismatches: 14
Query Match: 91.08% Indels: 0
DB: 10 Gaps: 0

US-10-764-259-13 (1-306) x ACC43342 (1-1243)

Qy 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys
Db 150 ATGCCGAGAGCGGAGATCGATCGTCGATCGAGCAGCTGATGGAGTGC
Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa
Db 210 TCCGAGGCGGAGGTGAAGACGCTGTGCGAGCAAGCGGCGGATCTGGT
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln
Db 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln

Db 270 AATGTTACGCGGTTAAGTGTCCGCTACCGTCTGCGGCGACATCCACGGCCAGTTTTCAC 329

Qy 61 AspleuileGluLeuPheArgileGlyLysAlaProAspThrAsnTyrLeuPheMet 80

Db 330 GATCTGATTAGCTTTTAAAGATCGGTGTTCTTCGCTCGACCAATATCTCTTCATG 389

Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100

Db 390 GGCAATTACGTAGATCGAGGGTATTATTCTCTGGAGACAGTCTCGCTCTTGGTAGCACTC 449

Qy 101 LysValArgTyrArgAspArgIleThrileLeuArgGlyAsnHisGluSerArgGlnIle 120

Db 450 AAAGTTCGTACAGATAGGCTTACCATCTTAAGAGGGATTCAGAAAGCGCCAAAT 509

Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140

Db 510 ACTCAAGTGTATGATTTTATGATGAGTGTCTGAGAAAATATGGAATATGTAATGTCTGTG 569

Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160

Db 570 AAACACATTCACGTGACCTTTTGAATTATCTCTTACAGCTCTCATCGAGATCAGGTT 629

Qy 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180

Db 630 TTCGTGTTACATGAGGGCTCTCACCTTCTTTAGATACACTTGACACATCCGTTCTCTA 689

Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200

Db 690 GATCGAATCCAAAGAGTTCCACATGAAGGACTATGTGTGATCTGTTATGTCGATCCA 749

Qy 201 AspAspArgCysGlyTrpGlyLeuSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220

Db 750 GATGATCATCGGTGCGGGAATATCTCTCTGCGCGAGGCTACACGTTTCGGAACAAGAT 809

Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240

Db 810 ATCGTACTCAGTTTAAACACACCATGAGCTCAGTCTGATCTCAAGAGCACACCACTT 869

Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260

Db 870 GTCATGAAGGTATAATTGTTGCGCAAGAAAGACGTTGTGACTGTCTTTAGCGCCCA 929

Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280

Db 930 AACTATTCTACCGATGCGGCAACATGCTGCTATTCTAGATAGACGAGAACATGGAC 989

Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300

Db 990 CAGAACTTCCTTCAGTTCGATCCAGCCCAAGTCAAGTAGAACCCGAAACTACACGCA 1049

Qy 301 ThrProAspTyrPheLeu 306

Db 1050 ACTCCAGATTACTTTTGG 1067

RESULT 7

ID ADX64434 standard; cDNA; 1732 BP.

AC ADX64434;

XX

XX 21-APR-2005 (first entry)

DT

XX

DE Plant full length insert polynucleotide seqid 35277.

XX

KW plant protectant; plant growth regulant; gene therapy; plant;

KW recombinant DNA construct; physical array; plant breeding marker;

KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;

KW growth rate; cell cycle pathway; disease resistance;

KW galactomannan production; lignin production; plant growth regulator;

KW yield; plant growth; plant development; seed oil; protein yield;

XX protein content; gene; ss.

OS Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVU/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABAS/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y.

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant to cold, heat, drought, herbicides, extreme osmotic conditions pests, for conferring increased resistance to plant disease improving yield.

XX Claim 1; SEQ ID NO 35277; 15pp; English.

XX The invention describes a recombinant DNA construct compris. polynucleotide consisting of a sequence encoding an amino a. available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The p. of the invention are also useful in physical arrays of mole. plant breeding markers. The recombinant DNA construct is us. improving plant tolerance to cold, heat, drought, herbicide. osmotic conditions, pathogens or pests, for manipulating gro. plant cells by modification of the cell cycle pathway, for increased resistance to plant disease, for producing galact. lignin or plant growth regulators, for increasing the rate. recombination in plants, for improving yield by modification. photosynthesis or carbohydrate, nitrogen or phosphorus use. or by providing improved plant growth and development under stress condition or for modifying seed oil or protein yield content. This sequence represents a plant full length inser. polynucleotide that can be used in the recombinant DNA consi. invention.

XX

SQ Sequence 1732 BP; 442 A; 392 C; 457 G; 441 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.75e-162 Length: 1732

Score: 1518.00 Matches: 272

Percent Similarity: 96.41% Conservative: 23

Best Local Similarity: 88.89% Mismatches: 11

Query Match: 90.90% Indels: 0

DB: 13 Gaps: 0

US-10-764-259-13 (1-306) x ADX64434 (1-1732)

Qy 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys

Db 222 ATGCCGTGCGACGCGGATCTGGACACACAGATCTCGCAGCTGCGGGATTG

Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal

Db 282 CCGAGGTGGAGGTCAAGACCTATGCGAGAGCAAGGCGATCCTCAT

Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly

Db 342 AACGTACAGCCGCTGCGCTGCCGCTCACTGTGTGCGGCGACATCCACGG

Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr

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Qy      81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerIleuLeuValAlaLeu 100
Db      462 GCGGATTAGCTGACCGTGGCTACTACTCTGTGGAGAGCTGTCTGTGTGTAGTGGCTCTTA 521
Qy      101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db      522 AAAGTACGTTATAGACAGACAGATCAATATTGAGAGGAAATCATGAGAGCAGACAAATA 581
Qy      121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyr 140
Db      582 ACTCAAGTGTATGGCTTCTATCATGAATCTCTCGGAAATATGGAATCGAAATGCTGTGG 641
Qy      141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db      642 AAGTACTTTACAGACTGTGTTGATTATTTGGCTCTCACAGCTCTTATAGAAAACAGATC 701
Qy      161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db      702 TTCTGCCTACATGGTGGTCTCTCTCCATCACTGGATACATTGGATAATATCCGCGCCCTT 761
Qy      181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyrSerAspPro 200
Db      762 GATCGCATACAAGAGTCCCATCAATGAAGGACCTATGTGTGATCTTTTGTGGTCTGACCCA 821
Qy      201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db      822 GATGACCGATGGTGGTGGGAATTTCCACCAAGGGTGTGGATACACATTTGGCCCAAGAT 881
Qy      221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
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Qy      241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPheSerAlaPro 260
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Qy      261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
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Qy      281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
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Db      1122 ACACCAAGACTACTTTTGT 1139
RESULT 8
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ID AAC40149 standard; DNA; 1267 BP.
XX
AC AAC40149;
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27232.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; 5S.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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Alignment Scores:

Pred. No.: 5.07e-162 Length: 1267
Score: 1514.00 Matches: 273
Percent Similarity: 94.77% Conservative: 17
Best Local Similarity: 89.22% Mismatches: 16
Query Match: 90.66% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x AAC40149 (1-1267)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCY:
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DB 159 ATGCGTCAACGGAGATCTCGACGTCAGATCGAACAGCTAATCGAGTG
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa:
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DB 219 GGTAAGCAGACGCGAAGATCCTTTGCCATCAAGCTAAAGCGATTCTCGT
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DB 279 AATGTTCAACCGGTAAAGTGCCGGTTACGGTATGCCGCGATATCCATGG:
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy:
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DB 399 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTATT
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AT 338

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IG 458

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PR	18-JUN-1999	99US-0139458P
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PR	18-JUN-1999	99US-0139461P
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PR	18-JUN-1999	99US-0139750P
PR	18-JUN-1999	99US-0139763P
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PR	22-JUN-1999	99US-0139899P
PR	22-JUN-1999	99US-0140353P
PR	23-JUN-1999	99US-0140354P
PR	24-JUN-1999	99US-0140695P
PR	28-JUN-1999	99US-0140823P
PR	29-JUN-1999	99US-0140991P
PR	30-JUN-1999	99US-0141287P
PR	01-JUL-1999	99US-0141842P
PR	02-JUL-1999	99US-0142154P
PR	02-JUL-1999	99US-0142055P
PR	06-JUL-1999	99US-0142390P
PR	08-JUL-1999	99US-0142803P
PR	30-JUN-1999	99US-0144085P
PR	16-JUL-1999	99US-0144086P
PR	19-JUL-1999	99US-0144325P
PR	19-JUL-1999	99US-0144331P
PR	19-JUL-1999	99US-0144332P
PR	19-JUL-1999	99US-0144333P
PR	19-JUL-1999	99US-0144334P
PR	19-JUL-1999	99US-0144335P
PR	20-JUL-1999	99US-0144352P
PR	20-JUL-1999	99US-0144632P
PR	21-JUL-1999	99US-0144884P
PR	21-JUL-1999	99US-0144814P

PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147933P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156559P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.

PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 2,21e-161 Length: 1422
Score: 1509.00 Matches: 269
Percent Similarity: 95.75% Conservative: 24
Best Local Similarity: 87.91% Mismatches: 13
Query Match: 90.36% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x AAC46572 (1-1422)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys; 20
DB 217 ATGCCGTGCGACGGGGATCTGGACCGGAGATCGCGAGCTGCGCGAGCTG; 276
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal; 40
DB 277 CCCGAGCGGAGGTCAGGGCGCTCTGCGAGCAGGCCAAGGCCATCCTTAT; 336
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly; 60
DB 337 AACGTGCAGCCGTGCGCTGTCTGTACCCGTCTGTGGCGACATCCACGG; 396
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy; 80
DB 397 GACCTCATCGAGCTCTCCCGCATCGCGCGACGCTCCCGACACCACTA; 456
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu; 100
DB 457 GCGGACTAGCTCGATCGTGGCTACTATTCACTCGAAACAGTTTCTCTGTT; 516
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe; 120
DB 517 AAAGTCCGTTACAGAGATAGAATTACAATACTTAGAGGAAATCATGAGAG; 576
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl; 140
DB 577 ACTCAAGTATATGGCTTCTATGATGAATGCTTAGAAAAATATGGAATGCG; 636
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGly; 160
DB 637 AAGTATTTTACAGACTTGTGTTGATTTTGGCTCTCTCACAGCTCTTATAGA; 696
QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIle; 180
DB 697 TTCTGTCTTCAATGGTGGCTCTCTCCGTCTATTGGACACGTTGGATAATAT; 756
QY 181 AspArgIleGlnGluValProHisGlyGlyProMetCysAspLeuLeuTr; 200
DB 757 GATCGGTACAGGAGGTTCCTCATGAGGAGCCCATGTGTGATCTTTGTG; 816
QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh; 220
DB 817 GATGACCGATGTGGTGGGAATTTTCCCAAGAGGAGCAGGTTACACATT; 876

[illegible]

PR 09-AUG-1999;	99US-0147935P.	PR	Query Match:	90.30%	Indels:	0	eu 20	
PR 10-AUG-1999;	99US-0148171P.	PR	DB:	3	Gaps:	0		
PR 11-AUG-1999;	99US-0148319P.	PR	US-10-764-259-13 (1-306) x AAC43368 (1-921)					TA 60
PR 12-AUG-1999;	99US-0148341P.	PR	QY	1	MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCy			
PR 13-AUG-1999;	99US-0148565P.	PR	DB	1	ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTC			
PR 13-AUG-1999;	99US-0148684P.	PR	QY	21	SerGluLeuGluValLysAsnLeuCysAspGlnAlaAargThrIleLeuVa		rp 40	
PR 16-AUG-1999;	99US-0149368P.	PR	DB	61	GGTGAAGCAGACGTAAGATCTTTGGCATCAAGCTAAAGCGATTCTTGT			
PR 17-AUG-1999;	99US-0149175P.	PR	QY	41	AsnValGlnProValLysCysProValThrValCysGlyAspIleHisG1		AT 120	
PR 18-AUG-1999;	99US-0149426P.	PR	DB	121	AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATCGCGGATATCCATGC		is 60	
PR 20-AUG-1999;	99US-0149722P.	PR	QY	61	AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy			
PR 20-AUG-1999;	99US-0149723P.	PR	DB	181	GACCTAATTGAGCTATTTCGTATTGGTGGTAATGCTCCTGATCTAATTA		AT 180	
PR 20-AUG-1999;	99US-0149929P.	PR	QY	81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe		et 80	
PR 23-AUG-1999;	99US-0149902P.	PR	DB	241	GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTAT			
PR 23-AUG-1999;	99US-0151066P.	PR	QY	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe		TA 300	
PR 27-AUG-1999;	99US-0151066P.	PR	DB	301	AAGGTGCGTTACAGGGACAGACTTACGATCTCGCAGGGAATCATGAGAG		le 120	
PR 30-AUG-1999;	99US-0151303P.	PR	QY	121	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl			
PR 31-AUG-1999;	99US-0151438P.	PR	DB	361	ACACAAGTCTATGGTTTTTATGACGAATGCTTTGAGGAAATACGGAATGC		TT 360	
PR 01-SEP-1999;	99US-0151930P.	PR	QY	141	LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleG1		rp 140	
PR 07-SEP-1999;	99US-0152363P.	PR	DB	421	AAGTATTTTACGGACCTTTTTCGATTATCTCCTCTTACAGCACTCATAGA			
PR 10-SEP-1999;	99US-0153070P.	PR	QY	161	PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI1		IT 480	
PR 13-SEP-1999;	99US-0153758P.	PR	DB	481	TTCTGTTTGCATGGAGGCCCTTTACCTTCTCTGGTACTCTTGACAATAT		eu 180	
PR 15-SEP-1999;	99US-0154018P.	PR	QY	181	AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr			
PR 16-SEP-1999;	99US-0154039P.	PR	DB	541	GATCGAATAAAGAGGTTCCACACAGAGCAATGTCCGATCTACTCTC		ro 200	
PR 20-SEP-1999;	99US-0154779P.	PR	QY	201	AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh		CC 600	
PR 22-SEP-1999;	99US-0155139P.	PR	DB	601	GACGATCGTTGTGGATGGGGAATATCTCCTCGTGTGCTGTACACGT		sp 220	
PR 23-SEP-1999;	99US-0155486P.	PR	QY	221	IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaAargAl			
PR 24-SEP-1999;	99US-0155659P.	PR	DB	661	ATTGCTACTAGTTTAAATCAATGAAGTGAAGTCTGATCTCAGAGAC		eu 240	
PR 28-SEP-1999;	99US-0156458P.	PR	QY	241	ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPh		IT 720	
PR 29-SEP-1999;	99US-0156596P.	PR	DB	721	GTAATGGAAGGCTATAATTGGTGTGAGGAAAGAACAGTAGTACAGTGT		ro 260	
PR 04-OCT-1999;	99US-0157117P.	PR	QY	261	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG1			
PR 05-OCT-1999;	99US-0157753P.	PR	DB	781	AACTACTGTTTACAGATGTGGAACATGCCCCCAATTTCTTGAGATTGGAGA		CG 780	
PR 06-OCT-1999;	99US-0157865P.	PR	QY	281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa		sn 280	
PR 07-OCT-1999;	99US-0158029P.	PR	DB	841	CAGAACTTCTTCAATTCGATCCAGCACTTAGACAACTCGAACCCGATAC		AA 840	
PR 08-OCT-1999;	99US-0158232P.	PR	QY	301	ThrProAspTyrPheLeu 306		ys 300	
PR 12-OCT-1999;	99US-0158369P.	PR	DB	901	ACCCCTGATTATTTTGG 918		AG 900	
PR 13-OCT-1999;	99US-0159293P.	PR	QY	RESULT 12				
PR 13-OCT-1999;	99US-0159294P.	PR	DB	ABZ12900				
PR 14-OCT-1999;	99US-0159329P.	PR	QY	ABZ12900 standard; DNA; 921 BP.				
PR 14-OCT-1999;	99US-0159330P.	PR	DB	XX				
PR 14-OCT-1999;	99US-0159331P.	PR	QY					
PR 14-OCT-1999;	99US-0159637P.	PR	DB					
PR 14-OCT-1999;	99US-0159638P.	PR	QY					
PR 18-OCT-1999;	99US-0159584P.	PR	DB					
PR 21-OCT-1999;	99US-0160741P.	PR	QY					
PR 21-OCT-1999;	99US-0160767P.	PR	DB					
PR 21-OCT-1999;	99US-0160768P.	PR	QY					
PR 21-OCT-1999;	99US-0160770P.	PR	DB					
PR 21-OCT-1999;	99US-0160814P.	PR	QY					
PR 21-OCT-1999;	99US-0160815P.	PR	DB					
PR 22-OCT-1999;	99US-0160980P.	PR	QY					
PR 22-OCT-1999;	99US-0160981P.	PR	DB					
PR 22-OCT-1999;	99US-0160989P.	PR	QY					
PR 22-OCT-1999;	99US-0160989P.	PR	DB					
PR 25-OCT-1999;	99US-0161404P.	PR	QY					
PR 25-OCT-1999;	99US-0161405P.	PR	DB					
PR 25-OCT-1999;	99US-0161406P.	PR	QY					
PR 26-OCT-1999;	99US-0161359P.	PR	DB					
PR 26-OCT-1999;	99US-0161360P.	PR	QY					
PR 26-OCT-1999;	99US-0161361P.	PR	DB					
PR 28-OCT-1999;	99US-0161920P.	PR	QY					
PR 28-OCT-1999;	99US-0161992P.	PR	DB					
PR 28-OCT-1999;	99US-0161993P.	PR	QY					
PR 29-OCT-1999;	99US-0162142P.	PR	DB					
Alignment Scores:								
Pred. No.:	1,578-161	Length:	921					
Score:	1508.00	Matches:	272					
Percent Similarity:	94.44%	Mismatches:	17					
Best Local Similarity:	88.89%	Conservative:	17					

AC ABZ12900;
 XX 21-JAN-2003 (first entry)
 DT
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 705.
 DE
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 KW
 XX Arabidopsis thaliana.
 OS
 XX WO200216655-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 24-AUG-2001; 2001WO-US026685.
 PF
 XX 24-AUG-2000; 2000US-0227866P.
 PR
 XX 26-JAN-2001; 2001US-0264647P.
 PP
 XX 22-JUN-2001; 2001US-0300111P.
 PS
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 DR
 XX Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 PT
 XX Claim 144; SEQ ID NO 705; 577pp + Sequence Listing; English.
 PS
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 921 BP; 252 A; 183 C; 225 G; 261 T; 0 U; 0 Other;

Alignment Scores:
 Pred. NO.: 1.57e-161 Length: 921
 Score: 1508.00 Matches: 272
 Percent Similarity: 94.44% Conservative: 17
 Best Local Similarity: 88.89% Mismatches: 17
 Query Match: 90.30% Indels: 0
 DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x ABZ12900 (1-921)

QY 1 MetProserTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
 DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGAAGCGGTTA 60
 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluIleTrp 40
 DB 61 GGTGAAGCAGACGTCGAAGATCTCTTCGATCAAGCTAAAGCGAATTCGTTGAGGAATAT 120
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlnPheHis 60
 DB 121 AATGTTCAACCGGTTAAGTGTCGGTACGGATGCGGCGATATCCATGGCCAGTTTAT 180
 QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
 DB 181 GACCTAATTGAGCTATTCGTATTGGTGTGTAATGCTCTCGTACTAATTAACCTCTTCATG 240

QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
 DB 241 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAAAGTCTCTCTATT 300
 QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe: 120
 DB 301 AAGGTGGTTACAGGACAGACTTACGATCTCTCGAGGGAATCATGAGAG 360
 QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgIlyTyrGlyAsnAl: 140
 DB 361 ACACAAGTCTATGCTTTTATGACGAATGCTTGAGGAATACGGAATGCG 420
 QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGlu 160
 DB 421 AAGTATTTTACGGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGA 480
 QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
 DB 481 TTCTGTTTGCATGAGGCGCTTTCACCTTCTCTGGTACTCTTGACAATAT 540
 QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp 200
 DB 541 GATCGAATACAAAGAGTTCCACACGAAGGACCAATGTGCGATCTACTCTG 600
 QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPhe 220
 DB 601 GACGATCGTGTGATGGGGAATATCTCTCGTGGTGTGTTACACGTT 660
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl: 240
 DB 661 ATTGCTACTCAGTTTAAATCATAAACATGGACTGAGTCTGATCTCAAGAGC 720
 QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhe 260
 DB 721 GTAATGGAAGCTATATATTGGTGTGAGGAAAGAACGTAGTGCACAGTGT 780
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGlu 280
 DB 781 AACTACTGTTACAGATGTGGAACATGCGCCCAATTTCTTGAGATTGGAGA 840
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa: 300
 DB 841 CAGAACTTCTTCAATTGATTCGAGCTCAGCACTAGACAAAGTCGAACCGATAC 900
 QY 301 ThrProAspTyrPheLeu 306
 DB 901 ACCCTGATTATTTT 918

RESULT 13
 AAC44779
 ID AAC44779 standard; DNA; 1344 BP.
 XX
 AC AAC44779;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Zea mays DNA fragment SEQ ID NO: 44101.
 XX
 KW Hybridisation assay; genetic mapping; gene expression contr
 KW protein identification; signal transduction pathway; metabo
 KW promoter; termination sequence; corn; ss.
 XX Zea mays subsp. mays.
 OS
 XX EP1033405-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-00301439.
 PF
 XX 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.

way;

PR	23-MAR-1999;	99US-0125788P.	PR	16-JUL-1999;	99US-0144085P.
PR	25-MAR-1999;	99US-0126264P.	PR	16-JUL-1999;	99US-0144086P.
PR	29-MAR-1999;	99US-0126785P.	PR	19-JUL-1999;	99US-0144335P.
PR	01-APR-1999;	99US-0127462P.	PR	19-JUL-1999;	99US-0144331P.
PR	06-APR-1999;	99US-0128234P.	PR	19-JUL-1999;	99US-0144332P.
PR	08-APR-1999;	99US-0128714P.	PR	19-JUL-1999;	99US-0144333P.
PR	16-APR-1999;	99US-0129845P.	PR	19-JUL-1999;	99US-0144334P.
PR	19-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-0144335P.
PR	21-APR-1999;	99US-0130449P.	PR	20-JUL-1999;	99US-0144352P.
PR	23-APR-1999;	99US-0130510P.	PR	20-JUL-1999;	99US-0144632P.
PR	23-APR-1999;	99US-0130891P.	PR	20-JUL-1999;	99US-0144884P.
PR	28-APR-1999;	99US-0131449P.	PR	21-JUL-1999;	99US-0144814P.
PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145086P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	04-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145085P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145089P.
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PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.: 7,58e-161 Length: 1344
Score: 1504.00 Matches: 269
Percent Similarity: 95.10% Conservative: 22
Best Local Similarity: 87.91% Mismatches: 15
Query Match: 90.06% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x AAC44779 (1-1344)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysLysProLeu 20
DB 229 ATGCGGTGCGACGGGATCTGGACCGGCAGATCGCGCAGCTCGCGACTGCGAAGTACCTG 288
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
DB 289 CCGGAGCGGAGGTCAAGGTGCTCTCGGAGCGGCAAGGCCATCTCTATGGAGGAATGG 348
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 349 AACGTGACGCGCGTGGCTGCGCCCGTACCGTCTCGCGGACATCCACGGCCAGTTCTAT 408
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrIleuPheMet 80
DB 409 GACCTCATCGAGCTCTTCGCGATCGCGCGAGCTCCCGACCAACTACCTCTTCATG 468
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 469 GCGGACTAGTCGTCGTGGCTATTATTCAGTTGAAACGGTTTCTCTGTAGTACTTGG 528
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIle 120
DB 529 AAAGTCCGTACAGAGATGAAATTAACAATCTCGAGGAAATCATGAGACGACAAATC 588
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrCysAsnAlaAsnValTrp 140
DB 589 ACTCAAGTGTACGGCTTCTATGATGAATCTTAAGAAATATGGAATGCAAAATGTATGG 648
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 649 AAGTATTTTACAGACTTGTTCATGATTATTTGCTTCACAGCTCTTATAGAAATCAGTTC 708

QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIle, 180
DB 709 TTCTGTCTTCATGGAGGCTCTCTCCGTCATTGGACACATTGGATAACAT 768
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp 200
DB 769 GATGCATACAGGAGGTACCTCATGAAGAGCCCATGTGTGATCTTTTGTG 828
QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPhe 220
DB 829 GATGACCGATGTGGTGGGAATTTTCAACCAGAGGAGCAGGTACACATT 888
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla, 240
DB 889 ATTGCACAGCAGTTTCAACCATACAAATGGTCTCTCTCTCATTTCAAGGGC 948
QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPhe 260
DB 949 GTAATGGAAGGATTTAATTTGGTCCAGATGAAGATGTAGTCACAGTCTTT 1008
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly 280
DB 1009 AATTACTGTTACCGCTGTGGTAACATGCTGCTATTCTTGAATCGGGAG 1068
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300
DB 1069 CAGAACTTCTTCAATTCACCCCGCACCTCGGCAAAATTGAGCCAGACAC 1128
QY 301 ThrProAspTyrPheLeu 306
DB 1129 ACCCAGACTACTTCTG 1146

RESULT 14

ABZ12766
ID ABZ12766 standard; DNA; 924 BP.
XX AC ABZ12766;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 571.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2000; 2000US-0227866P.
XX PR 26-JAN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX PA (SCRI) SCRIPPS RES INST.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Krepis J, Wang X, Zhu T;
XX DR WPI; 2002-304127/34.
XX PT Identifying a stress condition to which a plant cell has been
XX PS Claim 144; SEQ ID NO 571; 577pp + Sequence Listing; English
XX CC The invention relates to identifying a stress condition to which
XX CC cell has been exposed, comprising: (a) contacting nucleic acid
XX CC representative of expressed polynucleotides in the plant cell
XX CC array or probes representative of the plant cell genome; and

ad and
plant
in

CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 924 BP; 246 A; 183 C; 212 G; 283 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	4, 75e-160
Score:	1495.00
Percent Similarity:	95.41%
Best Local Similarity:	87.87%
Query Match:	89.52%
DB:	6
Length:	924
Matches:	268
Conservative:	23
Mismatches:	14
Indels:	0
Gaps:	0

US-10-764-259-13 (1-306) x ABZ12766 (1-924)

QY	2	ProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysIysProLeuSer	21
Db	7	CGCGGACCGGAGATATCATCGTCAGATCAGCAGCTTATGAGTGTAAAGCGTTATCT	66
QY	22	GluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleIeuValGluGluTrpAsn	41
Db	67	GAACCGGAGTGAAGATGTTGTGAGCACCCAAGACGATCTTGTGGAAGAGTATAAT	126
QY	42	ValGlnProValIysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAsp	61
Db	127	GTTCAACCGGTTAANTGTCGCGTTACCGTCTCGCGTGATATCACGGCCAAATTTACGAT	186
QY	62	LeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsnTyrIleuPheMetGly	81
Db	187	CTAATCGAGCTTTTCGTATCGGTCTCTCTCTCATATAATATCTTTTCATGGCT	246
QY	82	AspTyrValAspArgGlyTyrTyrSerValGluThrValSerIleuValAlaLeuLys	101
Db	247	GAATTATGTTGATCGAGGGTATTATTCTGTGGAGACAGTCTCACTTTGGTAGCACTGAA	306
QY	102	ValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThr	121
Db	307	GTTCTGTACAGGATAGACTTACTATCTTAAGAGGGAATCATGAAAGCCGTCAATTACT	366
QY	122	GlnValTyrGlyPheTyrAspGluCysLeuArgIysTyrGlyAsnAlaAsnValTrpLys	141
Db	367	CAAGTGTATGGGTTTTATGATGAATGTTTGAGGAAATATGAAATGCTAATGTATGGAAG	426
QY	142	TyrPheThrAspLeuPheAspTyrIleuProIeuThrAlaIleuIleGluHisGluIlePhe	161
Db	427	CACCTTCACGTATCTTTTGGATTATCTTCCACTTACAGCTCTTATTGAGAGTCAAGTTTC	486
QY	162	CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAsp	181
Db	487	TGTTTACATGAGGACTTTCACCTCTTTAGATACATCTGCACACATCCGATCTTTAGAT	546
QY	182	ArgIleGlnGluValProHisGluGlyProMetCysAspLeuIeuTrpSerAspProAsp	201
Db	547	CGAATTCAAGAGGTTCCACATGAAGGACCAATGTGTATCTCTTATGGTCTGATCCAGAT	606
QY	202	AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIle	221
Db	607	GACCGATCGGTTGGGGAATATCTCTGTGTGTCAGGCTACACTTTCGGACAAGATATC	666
QY	222	AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuVal	241
Db	667	GCTACTCAGTTTAACCAACCAATGGACTCTCTCTGATTTCAAGAGCACAATCAACTGTTC	726
QY	242	MetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsn	261
Db	727	ATGGAAAGTTTTAAATTTGGTGCAGAAGAAGAACTGTGACTGTATTATAGGCCCAAC	786

Qy	262	TyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThr	
Db	787	TATTGCTACCGTTGTGGCAACATGGCTGCGATTCTAGAGATCGGTGAGACA	
Qy	282	SerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValTh	
Db	847	AAATTCTCTTCAGTTTGATCCAGCTCCACGTCAGTCGAACCGGAAACCA	
Qy	302	ProAspTyrPheLeu 306	
Db	907	CCAGATTATTTTGTG 921	
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XX	AC	AAC42354;	
XX	AC		
XX	DT	17-OCT-2000 (first entry)	
XX	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 35235.	
XX	XX	Hybridisation assay; genetic mapping; gene expression contr	
KW	KW	protein identification; signal transduction pathway; metabo	
KW	KW	promoter; termination sequence; ss.	
XX	XX		
OS	OS	Arabidopsis thaliana.	
XX	XX		
PN	PN	EP1033405-A2.	
XX	XX	06-SEP-2000.	
XX	XX	25-FEB-2000; 2000EP-00301439.	
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 31-AUG-1999; 99US-0151438P.
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PR 10-SEP-1999; 99US-0153070P.
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PR 15-SEP-1999; 99US-0154018P.
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Alignment Scores:
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Matches:
Conservative: 23

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DB	253	GAACCGAGGTGAAGATGTTGTGTGACGACGCAAGACGATCTCTGTGGAGAGTATAAT	312
QY	42	ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAsp	61
DB	313	GTTCAACCGGTTAAATGTCGCGTTACCGTCTCGCGGTATATCCACGCCCAATTTTACGAT	372
QY	62	LeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGly	81
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QY	102	ValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThr	121
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QY	122	GlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLys	141
DB	553	CAAGTGTATGGGTTTATGATGATGATGTTTGAGGAATATGGAATGCTAATGTATGGAAG	612
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QY	162	CysLeuHisGlyLysLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAsp	181
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QY	182	ArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAsp	201
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QY	202	AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIle	221
DB	793	GACCGATGCGGTTGGGGAATATCTCTCGTGTGCGAGGTACACTTTTCGACACAGATATC	852
QY	222	AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuVal	241
DB	853	GCTACTCAGTTTAACACACACCAATGGACTCTCTGATTTCAAGACACATCAACTGTCT	912
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QY	262	TyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGluThrMetAsnArg	281
DB	973	TATTTGCTACCGTTTGTGGCAACATGGCTGCGATTTCTAGAGATCGGTGAGAACATGGACC	1032
QY	282	SerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLysThr	301
DB	1033	AAATTCCTTCAGTTTGTATCCAGCTCCACGTCAGTCGAACTCGAACCCGAAACCACTCGC	1092
QY	302	ProAspTyrPheLeu	306
DB	1093	CCAGATTATTTTGTG	1107

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:25:12 ; Search time 3752 Seconds
(without alignments)
3815.791 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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Database :

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11: gb_gss3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1522	91.1	1283	4	CNS0ADRX BX813946 Arabidops
2	1515	90.7	1285	4	CNS0AD99 BX816399 Arabidops
3	1512	90.5	921	10	CL964875 OstrFC011
4	1508	90.3	1429	4	AY104802 Zea mays
5	1493	89.4	1278	4	CNS0ADNP BX813410 Arabidops
6	1491	89.3	1250	4	CNS0ADL7 BX814752 Arabidops
7	1478	88.5	1534	4	AY108657 Zea mays

ALIGNMENTS

RESULT 1	CNS0ADRX	1283 bp	mRNA	linear	EB-2004
LOCUS	Arabisopsis thaliana Full-length cDNA Complete sequ				Clone
DEFINITION	GSUFB49ZD06 of Flowers and buds of strain col-0 of thaliana (thale cress).				sis
ACCESSION	BX813946				
VERSION	BX813946.1 GI:42474404				
KEYWORDS	HTC; GSLT cDNA				
SOURCE	Arabisopsis thaliana (thale cress)				
ORGANISM	Arabisopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e				phyta; edons;
AUTHORS	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clef Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Scha Temple,G., Caboche,M., Weissenbach,J. and Salanoubat Whole Genome Sequence Comparisons and 'Full-Length' A Combined Approach to Evaluate and Improve Arabidop				uences: me
TITLE	Annotation				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1283)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National				ncage :
COMMENT	BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@cns.fr) Web : www.genoscope.cns.fr				cns.fr
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members full-length libraries construction : Temple G.				out

8	1428	85.5	1198	4	CNS0ADDDH	BX816
9	1427	85.4	1749	4	CR594899	-leng
10	1427	85.4	1758	4	CR624778	-leng
11	1427	85.4	1781	4	CR596427	-leng
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14	1427	85.4	1983	4	AY609733	scrof
15	1423	85.2	1274	4	CNS0ADBD6	idops
16	1411	84.5	1585	4	AY609732	scrof
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18	1398	83.7	1016	5	BU901162	COURT
19	1393	83.4	1508	4	CNS0FVWV	adon
20	1393	83.4	1684	4	CNS0FSV6	adon
21	1393	83.4	1770	4	CNS0FR02	adon
22	1393	83.4	1771	4	CNS0FZIX	adon
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26	1385	82.9	1371	4	CNS0A9F1	idops
27	1384	82.9	849	7	CO082158	Ea46K
28	1381	82.7	1718	4	AY104886	mays
29	1380.5	82.7	1298	4	CNS0ADNK	idops
30	1376	82.4	1496	4	CNS0FOF9	adon
31	1375	82.3	1717	4	CNS0FS80	adon
32	1372	82.2	906	7	CK278240	24318
33	1372	82.2	933	7	CV291986	CV291
34	1371	82.1	1583	4	AY811939	1-15m
35	1368	81.9	1483	4	AY104329	stoso
36	1367	81.9	1678	4	CNS0PF6B	mays
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44	1355	81.1	1265	4	CNS0G5JH	adon
45	1355	81.1	1461	4	AK090311	muscu

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

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ORIGIN

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US-10-764-259-13 (1-306) x CNS0ADRX (1-1283)

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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleValGluGluTrp 40
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DB 296 AATGTTACGCGGTGAAGTGTCTGTACCGTTTGGCGGATATTCAGCGCCAGTTTAT 355
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
DB 356 GACCTTATTGACCTTTCGTATCGTGGCAACGCTCCTGTACTTAACCTCTTCATG 415
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VERSION BX816399.1 GI:42473558
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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rosids; eurosids II; Brassicaceae; Brassicaceae; Arab
1 (bases 1 to 1285)
REFERENCE Castelli V., Aury J.M., Jallion O., Wincker P., Clep
Menard M., Cruaud C., Quetier F., Scarpelli C., Schu
Temple G., Caboche M., Weissenbach J. and Salanoubat
Whole Genome Sequence Comparisons and 'Full-length'
A Combined Approach to Evaluate and Improve Arabidop
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1285)
AUTHORS Genoscope.
JOURNAL Direct Submission
TITLE Submitted (18-NOV-2003) Genoscope - Centre National
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@ge
- Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members
full-length libraries construction : Temple G
Genoscope members carried out sequencing and annotat
V., Aury J.M., Jallion O., Wincker P., Menard M., Cr
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the
genome released by MIPS (Munich Information center f
Sequences). 5 prime and 3 prime are assembled with P
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FEATURES
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BX813410
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VERSION HTC; GSLT cDNA.
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SOURCE Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1278)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Best Local Similarity: 88.24% Mismatches: 17
Query Match: 89.40% Indels: 0
Gaps: 4
US-10-764-259-13 (1-306) x CNSOADNP (1-1278)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCy eu 20
Db 177 ATGCCGTGAAGCGAGATCTCGACCGTCAGATCGAGCAGCTGATGGAGTGT TA 236
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa rp 40
Db 237 TCGGAGGCGGATGTGAGGACGCTTTGCGATCAAGCGAGCGATCCTTGT : 296
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGl is 60
Db 297 AATGTTACGCGGTGAAGTGTCTGTATACCGTTTCGCGCGATATTTCACGG : 356
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy et 80
Db 357 GACCTTATTAGCTCTTTTCGTATCGTGGCAACCGCTCTGTATCTACTA :TG 416
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe eu 100
Db 417 GGAGACTATGTAGATCGTGGCTACTATTTCAGTAGAGACAGTTTCTCTATT TA 476
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
Db 477 AAGTGCATACAGGATAGACTTACATCTTACGAGGGAATCACGAGAG :TT 536
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl rp 140
Db 537 ACTCAAGTCTATGGTTTTTATGACGAATGCTTGAGGAAGTAGCGGAAATGC GG 596
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGl le 160
Db 597 AAGTATTTTACAGACCTTTTCGATTATCTTCTTACCAGCCCTCATAGA : 656
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIl eu 180
Db 657 TTCTGTTTGCATGAGGCGCTTTCACCTTCTCTGGATACTCTTTGATAATAT TG 716
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr ro 200
Db 717 GATCGGATACAGGAGGTTCCACAGAGGAGCTATGTGTGATTTATTATTC CT 776
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTrpPhe sp 220
Db 777 GATGATCGATGTGGATGGGAATATCTCCACGAGGTGCTGGTTATACATT AT 836
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
Db 837 ATCGCAGCTCAATTTAATAACAACAATGAGCTAAGTCTCATATCAAGAGC IT 896
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh ro 260
Db 897 GTCATGGGAAGGTTTAACTGTGTGAGGATGAAGATGGGTACTGTGTI CA 956
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl sn 280
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Db 957 AACATTGCTACCGGTGTGGAAACATTGCTGCATCTTAGAGATAGGAGATACATGGAG 1016
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 1017 CAAAACTTCTCCAGTTGATCCAGCTCTCTGACAAAGTTGAACCTGATACTACTCGGAAG 1076
Qy 301 ThrProAspTyrPheLeu 306
Db 1077 ACCCTGATTGTGTCTTG 1094
RESULT 6
CNSOADL7
LOCUS
DEFINITION
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
thaliana (thale cress).
ACCESSION
BX814752
VERSION
BX814752.1 GI:42474221
KEYWORDS
HTC; GSLT cDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicaceae; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 1250)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat M.
TITLE
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1250)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES
source
1..1250
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB92E04"
/tissue_type="flowers and buds"
/ecotype="Col-0"
/plasmid="pCMWSPORT 6"
complement(1..1250)
/gene="At1G59830"

ORIGIN
Alignment Scores:
Pred. No.: 6,67e-163 Length: 1250
Score: 1491.00 Matches: 270
Percent Similarity: 93.79% Conservative: 17
Best Local Similarity: 88.24% Mismatches: 19
Query Match: 89.28% Indels: 0
DB: 4 Gaps: 0

US-10-764-259-13 (1-306) x CNSOADL7 (1-1250)
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Db 181 ATGCCGTTAAACCGGAGATCTCGACCGTCAGATCGAACAGCTAAATGGAGTT 240
Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaThrIleLeuVal: 40
Db 241 GGTGAAGCAGACGCTGAAGATCTCTTGGCATCAAGCTAAAGCGATTCTTGT 300
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly: 60
Db 301 AATGTTCAACCGTTAAGTGTCCGGTTACGGTATGCCGGGATATCCATGG: 360
Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy: 80
Db 361 GACCTAATGAGCTATTTTCGTATTGGTGGTAAATGCTCTCTGATATAATTA: 420
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe: 100
Db 421 GGAGATTATGTAGATCTGGCTACTATTCTGTAGAAAACAGTCTCTCTATT: 480
Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe: 120
Db 481 AAGTGGGTTACAGGACGACACTTACGATCTCTGCGAGGAATCATGAGAG: 540
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl: 140
Db 541 ACACAAGTCTATGTTTTTATGACGAATGCTTGGAGAAATACGGAAATGCT: 600
Qy 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGly: 160
Db 601 AAGTATTTTACGGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGA: 660
Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle: 180
Db 661 TTCGTGTTGCAAGGAGCCCTTTCACCTTCTCTGGATCTCTTGACAAATAT: 720
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr: 200
Db 721 GATCGAATACAAGAGGTTCCACACAGGACCAATGTGCGATCTACTCTG: 780
Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh: 220
Db 781 GACGATCGTTGTGATGCGGAATATCTCTCTGCTGCTGCTGTACACGTT 840
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaAtqAl: 240
Db 841 ATTGCTACTCAGTTTAAATCATAACATGAGCTGAGTCTGATCTCAAGAGC: 300
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh: 260
Db 901 GTAATGAAGGCTATAATTTGGTGTGAGGAAAGAACGTTAGTGACAGTGT 960
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly: 280
Db 961 AACTACTGTTACAGATGTGGAACAATGCGCCCAATTTCTTGATTTGGAGA: 1020
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa: 300
Db 1021 CAGAACTTCTTCAATTGATCCAGCACTTAGACAAGTCAACCCGATAC: 1080
Qy 301 ThrProAspTyrPheLeu 306
Db 1081 ACCCTGATTATCTTTTG 1098
RESULT 7
LOCUS
DEFINITION
Zea mays PC0069598 mRNA sequence.
ACCESSION
AY108657
VERSION
AY108657.1 GI:21211829
KEYWORDS
HTC.

SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1534)
AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H., Jr.
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 1534)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 1534)
AUTHORS Coe, E.H.
JOURNAL Direct Submission
TITLE Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES
source
Location/Qualifiers
1..1534
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeGDB:633783"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN
Alignment Scores:
Pred. No.: 2,94e-161 Length: 1534
Score: 1478.00 Matches: 268
Percent Similarity: 94.81% Conservative: 24
Best Local Similarity: 87.01% Mismatches: 14
Query Match: 88.50% Indels: 2
Gaps: 0
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DB 192 ATGCGGTGCGACGGGATCTGGACCGGAGATCGCGAGTGGCGGACTGCAAGTACCTG 251
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLtrp 40
DB 252 CCCGAGGGGAGGTCAAGCGCTCTCGAGACGAGGCAAGGCCATCTTATGGAGAGTGG 311
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlnPheHis 60
DB 312 AACGTGACCGCGTGGTGGCCCGTCCCGTCTCGCGGAGGATCCACGGCCAGTCTAT 371
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnThrLeuPheMet 80

DB 372 GACCTCATCGAGCTCTTCCGCATCGCGGGGACTCTCCCGACACCAACTA
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe
DB 432 GGCAGCTACGTCGATCGTGCTATTATTTCAGTTGAAACAGATTTCTCTGT
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe
DB 492 AAAGTCGGTTACAGATAGATAATTACAATACTTAGAGGAATCATGAGAG
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl
DB 552 ACTCAAGTATATGCTCTCTATGATCAATGCTTAAAGAAAATATGGAATGC
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuLeG1
DB 612 AAGTATTTTACAGACTTGTGTTGATTTTTTGGCTCTCACAGCTCTTATAGA
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI1
DB 672 TTCTGTCTTCATGCTGGCTCTCTCCGTCATTGGACACATTGGATAATAT
QY 181 AspArgIleGlnGluValPro-HisGluGlyProMetCysAspLeuLeu1
DB 732 GATCGCGTACAGGAGTTCCTCCATGAAGGACCCATGTGTGATCTTTGT
QY 200 oAspAspArgCysGlyTrpGlyIleSerProArgGlyValaGlyTyrThrF
DB 792 AGATGACCGATGTGGATGGGAATTTCCACANGAGGACGAGTTACACAT
QY 220 pIleAlaGlnPheAsnHisThrAsnGlyLeuSerLeuValaAlaArgA
DB 852 CATTGGCAGCAGTTCACCATACAAATGGTCTTTCTCTCATTTCAAGGG
QY 240 uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValF
DB 912 TGTAATGAGAGGATTAATTTGGTGGCAGGATAAGAAATGTAGTCACAGTC1
QY 260 oAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG
DB 972 TAATTACTGTTTACCCTGTGTGTAACATGCTGCTATTCTTGAAATCGGGG
QY 280 nArgSerPheLeuGlnPheGluProAlaProArg-GlnSerGluProAsf
DB 1032 CCAGACTCTCTTCATTCACCCCGCACCTCGGGCAAATTTGAGCCAGAC
QY 300 YsThrProAspTyrPheLeu 306
DB 1092 AAACCCAGAGTACTTTCTG 1111
RESULT 8
CNS0ADDD 1198 bp mRNA linear
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequ
DEFINITION GSLTPGH57ZF10 of Hormone Treated Callus of strain cc
ACCESSION Arabidopsis thaliana (thale cress).
VERSION BX816593.1 GI:42474290
KEYWORDS Htc; GSLT_cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
rosids; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1198)
Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clef
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Scha
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat
Whole Genome Sequence Comparisons and 'Full-length'
A Combined Approach to Evaluate and Improve Arabidof
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1198)
phyta;
edons;
ences;
me


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QY 246 AsnTyrCysGlnAspLysAsnValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db 922 AACTGGTGCATGACCGGAATGAGTAAAGATTTTCAGTGTCTCCAACTATTGTTATCGT 981
QY 266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db 982 TGTGTGAACCAAGCTGCAATCATGAAGACTTGACGATACTCTAAATACTCTTTCTTGCAG 1041
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db 1042 TTTGACCCAGCACTCTGAGAGCGGAGCCACATGTTACTCTGTCGTACCCAGACTACTTC 1101
QY 306 Leu 306
Db 1102 CTG 1104

RESULT 12
CR619537
LOCUS 1830 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DM014YH02 of Fetal liver of Homo sapiens
(human).
ACCESSION CR619537
VERSION CR619537.1 GI:50500344
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1830)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1830)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1830
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM014YH02"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 3.45e-155 Length: 1830
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17
Query Match: 85.45% Indels: 0
Gaps: 4
DB:

US-10-764-259-13 (1-306) x CR619537 (1-1830)

QY 6 AspValAspArgGlnIleGluLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db 253 GAGCTGGACCACTGATCGACAGCTGACAGTGCAGAGCTGTCCGATCCAGGTC 312
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluThrProAsnValGlnProVal 45

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Db 313 AAGACCTCTCGAGAGCGCTAAAGAAATCCTGACAAAGAAATCCACCGT
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeu
Db 373 CGATGTCCAGTTACTGTCTGTGGAGATGTGATGGGCAATTTTCATGATCT
QY 66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAsp
Db 433 TTTAGAAATGGTGGCAATCACCAGATACAAATACTTGTGTTATGGGAGA
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa
Db 493 AGAGGATATTATTAGTTGAAACAGTACACTGCTTGTAGCTCTTAAAGGT
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGln
Db 553 GAACGATCACCATTCTTCGAGGGAATCATGAGAGCAGACAGATCACACA
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTyr
Db 613 TTCTATGATGATGTTTAAAGAAATATGGAATGCAATGTTTGGAAATP
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuLeuGluHisGluIlePheCys
Db 673 CTTTGTGACTATCTCTCTCTCACTGCTTGGTGGATGGCAGATCTTCTG
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr
Db 733 GGTCTCTCGCCATCTATAGATACACTGGATCATATCAGAGCACTTGTATCG
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAs
Db 793 GTTCCCATGAGGCTCCAAATGTGTGACTTGTGTGGTCCAGATCCAGATGA
QY 206 TrpGlyLeuSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl
Db 853 TGGGTATATCTCTCGAGAGCTGGTTACACCTTTGGGCAAGATATTTC
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValme
Db 913 AATCATGCCAATGCCCTCACGTTGGTGTCTAGAGCTCACCAGCTAGTGAT
QY 246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyr
Db 973 AACTGTGTGCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAACTP
QY 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe
Db 1033 TGTGTAACCAAGCTGCAATCATGGAACCTTGACGATACTCTAAATACTC
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPi
Db 1093 TTTGACCCAGCACCTCTGTAGAGCGGAGCCACATGTTACTCTGTCGTACCCC
QY 306 Leu 306
Db 1153 CTG 1155

RESULT 13
CR619537
LOCUS 1830 bp mRNA linear
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIK
enriched library, clone:2810407123 product:protein F
catalytic subunit, alpha isoform, full insert sequen
AK076110
ACCESSION AK076110.1 GI:26345081
VERSION AK076110.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muridae; Mus.
1
REFERENCE

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Db      911 AATCATGCCAATGGCGCTCACGTTGGTGTCCAGAGCTCACAGCTGGTGATGGAGGGATAT 970
Qy      246 AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db      971 AACTGGTCCCATGACCGGAAGCTAGTAAACAATTTTCAGTGTCTCCAAACTATTTGCTATCGT 1030
Qy      266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285
Db      1031 TGTGTGAACCAAGCTGCAATCATGGAACCTTGACGACACTCTTAAAGTATTTCTTTCTTCAG 1090
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db      1091 TTTGACCCAGCACTCGTAGAGCGGCGACACATGTCACCTCGTCGTACCCAGACTACTTC 1150
Qy      306 Leu 306
Db      1151 CTG 1153

RESULT 14
AY609733
LOCUS      AY609733      1983 bp      mRNA      linear      HTC 31-JAN-2005
DEFINITION Sus scrofa clone Clu_2818.scr.msk.pl.Contig3, mRNA sequence.
ACCESSION AY609733
VERSION   AY609733.1 GI:52351301
KEYWORDS HTC.
SOURCE    Sus scrofa (pig)
ORGANISM  Sus scrofa
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
           Sus.
REFERENCE 1 (bases 1 to 1983)
AUTHORS   Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M.
           and Schierup M.H.
TITLE      Comparative analysis of protein coding sequences from human, mouse
           and the domesticated pig
JOURNAL   (er) BMC Biol. 3 (1), 2 (2005)
PUBMED    15679890
REFERENCE 2 (bases 1 to 1983)
AUTHORS   Hornshoj,H., Bendixen,C. and Panitz,F.
TITLE      Direct Submission
JOURNAL   Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
           Institute of Agricultural Sciences, Research Centre Foulum, Postbox
           50, Tjele DK-8830, Denmark
FEATURES  Location/Qualifiers
           source          1..1983
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           misc_feature     1..1983
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                        alpha subunit"
ORIGIN

Alignment Scores:
Pred. No.:      3,86e-155      Length:      1983
Score:          1427.00      Matches:     252
Percent Similarity: 94.35%      Conservative: 32
Best Local Similarity: 83.72%      Mismatches:  17
Query Match:    85.45%      Indels:      0
DB:             4      Gaps:      0

US-10-764-259-13 (1-306) x AY609733 (1-1983)
Qy      6 AspValAspArgGlnIleGluLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db      254 GAGCTGGACCACTGGATCGAGCAGCTGAATGATGTCAGACAGCTGTCGAGTCCCGAGTCC 313
Qy      26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluThrAsnValGlnProVal 45
Db      314 AAGACCTCTTCGGAAGGCTTAAGAAATCTCTGACAAAAGAAATCCAACTGCAAGAGGTT 373
Qy      46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65

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Db      374 CGATGTCCAGTCACTGTCTGTGGAGATGTGCACGGGCAATTTTCATGATCT 433
Qy      66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAe 85
Db      434 TTTAGAATTGGTGCAAAATCACCAGATACGAAATTTACCTGTTTATGGGAGA 493
Qy      86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa 105
Db      494 AGAGGATATTATTCGGTTGAACACAGTTACTCTGCTTGTAGCTCTTAAGGT 553
Qy      106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGl 125
Db      554 GAACCCATCACCATTCCTTCGAGGAAATCATGAGAGCAGACAGATCACACA 613
Qy      126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTy 145
Db      614 TTCTATGATGAGTGTTTAAGGAAATATGGAATGCAATGTTTGGAAAT 673
Qy      146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCy 165
Db      674 CTTTTTGATTATCTCTCTCTCCTGATTCATGATGATGGCAGATCTTCTG 733
Qy      166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr 185
Db      734 GGCCTCTCACCATCCATAGATACACTGATGCATCACATCAGAGCATTGATCG 793
Qy      186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAe 205
Db      794 GTTCCCATGATGAGGTCCCAATGTGTGACTTGTGTTGGTTCAGATCCAGATGA 853
Qy      206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl 225
Db      854 TGGGGTATATCTCTCCAGGAGCTGGTTACACTTTTGGGCAAGATATTTC 913
Qy      226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe 245
Db      914 AATCATGCCAATGGCTCACGTTGGTGTCCAGAGCTCATCAGCTCGTGAT 973
Qy      246 AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTy 265
Db      974 AACTGGTGCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAACTA 1033
Qy      266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe 285
Db      1034 TGTGGGAACCAAGCTGCAATCATGGAACCTTGATGATCTCTAAAATACTC 1093
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
Db      1094 TTTGACCCAGCACCTCGCAGAGGGGAGCCACACAGTTACTCTGCTGACCCC 1153
Qy      306 Leu 306
Db      1154 CTG 1156

RESULT 15
CNS0ADB6
LOCUS      CNS0ADB6      1274 bp      mRNA      linear
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequ
           GSLTPGH22A06 of Hormone Treated Callus of strain cc
           Arabidopsis thaliana (thale cress).
ACCESSION BX816000
VERSION   BX816000.1 GI:42473421
KEYWORDS HTC; GSI, cDNA.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core e
           rosid; eurosoids II; Brassicales; Brassicaceae; Arab
           1 (bases 1 to 1274)
REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clef
AUTHORS   Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Scha
           Temple,G., Caboche,M., Weissensbach,J. and Salanoubat

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 9, 2005, 10:27:22 ; Search time 203 Seconds
(without alignments)
2679.477 Million cell updates/sec

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1670	100.0	1365	US-09-828-302-8
2	1427	85.4	1787	Sequence 8, Appli
3	1427	85.4	2181	Sequence 39, Appl
4	1427	85.4	2182	Sequence 17, Appl
5	1427	85.4	2566	Sequence 5543, Ap
6	1411	84.5	1522	Sequence 3, Appli
7	1411	84.5	1541	Sequence 5464, Ap
8	1411	84.5	1781	Sequence 590, App
9	1411	84.5	1843	Sequence 10, Appl

10	1411	84.5	2574	3	US-09-780-045-3	Sequ
11	1366	81.8	1721	3	US-09-190-976B-11	Sequ
12	1291	77.3	1134	3	US-09-487-558B-269	Sequ
13	1286	77.0	1110	3	US-09-614-221A-47	Sequ
14	1286	77.0	1110	3	US-09-487-558B-267	Sequ
15	1137.5	68.1	1339	3	US-09-949-016-2909	Sequ
16	1137.5	68.1	1360	3	US-09-825-497A-41	Sequ
17	1025	61.4	614	3	US-09-533-559-46	Sequ
18	978	58.6	936	3	US-09-614-221A-424	Sequ
19	973	58.3	1484	3	US-09-949-016-3862	Sequ
20	963.5	57.7	957	3	US-09-248-796A-4207	Sequ
21	958.5	57.4	912	3	US-09-916-338A-1	Sequ
22	804	48.1	447	3	US-09-828-302-3	Sequ
23	786	47.1	8263	3	US-09-248-796A-4206	Sequ
24	757	45.3	2163	3	US-09-825-497A-42	Sequ
25	739	44.3	1367	3	US-09-167-206-5	Sequ
26	739	44.3	1367	3	US-09-190-976B-9	Sequ
27	739	44.3	1396	3	US-09-949-016-1492	Sequ
28	736	44.1	3590	3	US-09-949-016-395	Sequ
29	736	44.1	3591	3	US-09-949-016-3213	Sequ
30	729.5	43.7	960	3	US-09-248-796A-4220	Sequ
31	701	42.0	459	3	US-09-300-958A-38	Sequ
32	696.5	41.7	783	3	US-09-248-796A-4241	Sequ
33	639	38.3	552	3	US-09-248-796A-4210	Sequ
34	629.5	37.7	2079	3	US-09-487-558B-273	Sequ
35	614.5	36.8	2133	3	US-09-487-558B-275	Sequ
36	589	35.3	13316	3	US-09-949-016-14651	Sequ
37	565	33.8	2064	3	US-09-949-016-4347	Sequ
38	565	33.8	5525	3	US-09-744-016A-20	Sequ
39	565	33.8	5555	3	US-09-744-016A-17	Sequ
40	565	33.8	6268	3	US-09-744-016A-4	Sequ
41	559	33.5	2257	2	US-08-452-722-6	Sequ
42	559	33.5	2257	2	US-08-404-731A-6	Sequ
43	559	33.5	2257	2	US-08-344-227-6	Sequ
44	559	33.5	2257	2	US-08-503-226B-6	Sequ
45	559	33.5	2257	3	US-08-721-458B-6	Sequ

ALIGNMENTS

RESULT 1
US-09-828-302-8
; Sequence 8, Application US/09828302
; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8

Alignment Scores:	2.32e-203	Length:	1365
Pred. No.:	1670.00	Matches:	306
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
US-10-764-259-13 (1-306) x US-09-828-302-8 (1-1365)			

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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
Db 131 TCGGAGTTGGAGGTGAGAACCTATGTGATCAAGCTCGAGCATCTTGTGTGAGGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 191 AACGTGCAGCCGTGAGTGTCTGTACGGTTTGGGTGACATCCATGGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsnTyrIleuPheMet 80
Db 251 GATCTCATCGAGCTTTTCGCATAGAGGCAAGGCCCGCCGACACGAACCTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrSerValGluThrValSerLeuLeuValAlaLeu 100
Db 311 GCGGCTATGTGGATCGTGGATATTATTCTGTGAGACTGTGTCTCTTATGTGGCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 371 AAGGTGCGGTATAGGATAGGATCACATCTTCGAGGGGAACCCAGCAGCAGCAGATT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db 431 ACGCAAGTATATGTTTCTATCATGAATGCCCTCGCGAAGTATGCAAAATGCGAAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGluHisGluIle 160
Db 491 AAGTACTTTCAGGATCTGTGTGACTTACTCTGCCTCTGACAGCTCTCATTTGAGCACGAGATT 550
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db 551 TTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACACATTAGATCATCATCGAGCCCTA 610
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 611 GATCGTATTCAGAAAGTCCGCGCACGAGGCCGCGATGTGTGATCTACTCTGGTCTGATCCA 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 671 GATGATCGTTGTGGATGGGGCAATTTCCACGAGGTGCCGGTTATACTTTTGGTCAAGAT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 731 ATTGCAGAGCAGTTCATATACATACCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGCTT 790
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
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QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
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QY 301 ThrProAspTyrPheLeu 306
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RESULT 2

US-09-300-958A-39
; Sequence 39, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas

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; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets ;  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/09/300,958A  
; CURRENT FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 1787  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-300-958A-39  
  
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Pred. No.: 4,49e-172 Length: 1787  
Score: 1427.00 Matches: 252  
Percent Similarity: 94.35% Conservative: 32  
Best Local Similarity: 83.72% Mismatches: 17  
Query Match: 85.45% Indels: 0  
DB: 3 Gaps: 0  
  
US-10-764-259-13 (1-306) x US-09-300-958A-39 (1-1787)  
  
QY 6 AspValaspArgGlnIleGluGlnLeuSerGluCysIysProLeuSerGln 1 25  
Db 207 GAGCTGGACCACTGGATCGAGCAGCTGAACGAGTGCAGCAGCTGTCCGA 1 266  
  
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnVal 1 45  
Db 267 AAGAGCTCTCGAGAGGCTAAAGAAATCTGCACAAAGAAATCCACGTT 1 326  
  
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeu 1 65  
Db 327 CGATGTCAGTTACTGTCTGTGGAGATGTGCATGGCAATTTTCATGATCT 1 386  
  
QY 66 PheArgIleGlyIysAlaProAspThrAsnTyrIleuPheMetGlyAsp 1 85  
Db 387 TTTAGAATTGTGGCAAAATCACCAGATACAAATTTACTTTGTATGGGAGA 1 446  
  
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVal 1 105  
Db 447 AGAGGATATTATTTCAGTTGAAACAGTTACACTGCTTTGTAGCTTTAAGGT 1 506  
  
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlu 1 125  
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QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyr 1 145  
Db 567 TTTCTATGATGAATGTTTAAAGAAATATGGAATGCAATGTTTGGAAATA 1 626  
  
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys 1 165  
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QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg 1 185  
Db 687 GGTCTCTCGCCATCTATAGATACACTGGATCATATCAGAGCAGCTTGTATCG 1 746  
  
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAsp 1 205  
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QY 206 TrpGlyIleSerProArgGlyValaGlyTyrThrPheGlyGlnAspIleAla 1 225  
Db 807 TGGGGTATATCTCTCTCGAGGAGCTGGTTACACCTTTTGGGCAAGATATTTCT 1 866
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QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
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Db 927 AACTGGTGCCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAAACTATTGTATCGT 986
QY 266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
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QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
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QY 306 Leu 306
Db 1107 CTG 1109
RESULT 3
US-09-780-049-17
; Sequence 17, Application US/097800049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 17
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1139)
US-09-780-049-17

Alignment Scores:

Pred. No.: 6,17e-172 Length: 2181
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17
Query Match: 85.45% Indels: 0
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US-10-764-259-13 (1-306) x US-09-780-049-17 (1-2181)

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QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluThrAsnValGlnProVal 45
Db 294 AAGACCTCTCGGAGGCTTAAGAAATCTTGACAAAGAAATCAACCTGCAAGAGGTT 353
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65
Db 354 CGATGTCCAGTTACTGTCTGTGGAGATGTGCATGGGCAATTCATGATCTCATGGAACGTG 413
QY 66 PheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
Db 414 TTTAGAATTGGTGGCAAAATCACCAGATCAAAATTAATCTGTTTATGGGAGATTATGTTGAC 473
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeuLysValArgTyrArg 105
Db 474 AGAGGATATTATTAGTTGAACAGTGTACCTGTGTAGCTCTTAAGGTTGCTTACCGT 533
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly 125

Db 534 GAACGCATCACCATTCTTCGAGGGAATCATGAGAGCAGACAGATCACACA
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaValTrpLysTyr
Db 594 TTTCTATGATGAATGTTTAAGAAATATGGAATGCAATGTTTGGAAATA
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys
Db 654 CTTTTTGACTATCTCTCTCACCTGCCTTGGTGGATGGGAGATCTTCTG
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg
Db 714 GGTCTCTCGCCATCTATAGATACACTGCGATCATATCAGAGCACTTGATCG
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAs
Db 774 GTTCCCATGAGGGTCCAATGTGTGACTTGTGTGGTCCAGATCCAGATGA
QY 206 TrpGlyIleSerProArgGlyValAlaGlyTyrThrPheGlyGlnAspIleAl
Db 834 TGGGGTATATCTCTCGAGGAGCTGGTTACACCTTTGGGCAAGATATTTTC
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe
Db 894 AATCATGCCAATGGCTCACCGTTGGTGTCTAGAGCTCACCAGCTAGTGAT
QY 246 AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyr
Db 954 AACTGGTGCCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAAACTA
QY 266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSe
Db 1014 TGTGTAAACCAAGCTGCAATCATCGAACTTGACGACTCTCTAAAATACTC
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPyr
Db 1074 TTTGACCCAGCACCTCGTAGAGCGAGCCACATGTTACTCGTGTGTCGTCACCCC
QY 306 Leu 306
Db 1134 CTG 1136

RESULT 4

US-09-949-016-5543
; Sequence 5543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5543
; LENGTH: 2182
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5543

Alignment Scores:
Pred. No.: 6,17e-172 Length: 2182
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17

S THEREOF


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Db      1679 AATCATGCCAATGGCTCAGTGTGCTGTAGAGCTCACCAGCTAGTGTATGGAGGATAT 1738
Qy      246 AenTTPCyGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCySTyrArg 265
Db      1739 AACTGGTGCATGACCGGAATAGTAGACGATTTTCAGTGTCCAAACTATTGTATCGT 1798
Qy      266 CysGlyAsnMetAlaAlaileMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db      1799 TGTGTGAACCAAGCTGCAATCATGCACTTGACGATCTCTAAATACTCTTTCTTGCAG 1858
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db      1859 TTTGACCCAGCACTCGTAGAGCGGACACATGTTACTCGTGTGACCCAGACTACTTC 1918
Qy      306 Leu 306
Db      1919 CTG 1921

RESULT 6
US-09-949-016-5464
; Sequence 5464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5464
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5464

```

```

Alignment Scores:
Pred. No.:      3 89e-170      Length:      1522
Score:          1411.00      Matches:      248
Percent Similarity: 93.69%      Conservative: 34
Best Local Similarity: 82.39%      Mismatches: 19
Query Match:      84.49%      Indels: 0
DB:              3          Gaps: 0

```

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US-10-764-259-13 (1-306) x US-09-949-016-5464 (1-1522)

Qy      6 AspValAspArgGlnleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db      32 GAGCTGGACCACTGGGTGCGAGCAGCTGAACGAGTGTAGCAGCTGAACGAGAACCAAGTG 91
Qy      26 LysAsnLeuCysAspGlnAlaArgThrleLeuValGluGluThrAsnValGlnProVal 45
Db      92 CGGAGCGCTGTGCGAGAGGCAAGGAAATTTTAAACAAAAGAAATCAATGTGCAAGAGGTT 151
Qy      46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65
Db      152 GTTGCCCTGTACTGTCTGTGGAGATGTGATGTGCAATTTTCAATGCTTATGGAATCTC 211
Qy      66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
Db      212 TTAGAATTTGGTGAATCAACCGATACAACTACTTATTATGCTGCTATGTAGAC 271
Qy      86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105
Db      272 AGAGGATATTATTAGTGGAGACTGTGACTCTTCTTGTAGCAATTAAGGTCGTTATCCA 331

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Qy      106 AspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIleThrGln 125
Db      332 GAACGCATTACAATATTGAGAGGAAATCACCAGAACCCACAAATTTACCCA 391
Qy      126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTyr 145
Db      392 TTTTATGATGAATGTCTCGAAAGTATGGAATGCCAACGTTTGGAAATA 451
Qy      146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGlyIlePheCys 165
Db      452 CTCCTTGAATATCTTCCACTTACAGCTTTAGTAGATGGACAGATATCTG 511
Qy      166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg 185
Db      512 GGCCTCTCTCCATCCATAGACACACTGGATCATATAGAGCCCTGGATCG 571
Qy      186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAs 205
Db      572 GTTCCACATGAGGCCCAATGTGTGATCTGTATGTCAGATCCAGATGA 631
Qy      206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl 225
Db      632 TGGGGTATTTCCACCACGCTGCTGGCTGCTACACATTTGGACAGACATTTTC 691
Qy      226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe 245
Db      692 AACCATGCCAATGCTCTCACACTGTTTCTCGTCCCAACAGCTTGTAAI 751
Qy      246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyr 265
Db      752 AATTGGTGTATGATCGGAATGTGTTACCATTTTTCAGTCGACCCCAATTA 811
Qy      266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe 285
Db      812 TGTGGGAACCAAGGCTGCTATCATGGAATTAGATGACACTTTTAAATATATTC 871
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
Db      872 TTTGACCCAGCGCTCGTCTGCTGGTGGAGCTCATGTATACCGGCGCACCCC 931
Qy      306 Leu 306
Db      932 CTA 934

```

```

RESULT 7
US-09-949-016-590
; Sequence 590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-590

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Alignment Scores:
Pred. No.:      3 96e-170      Length:      1541
Score:          1411.00      Matches:      248

```

S THEREOF

Percent Similarity:	93.69%	Conservative:	34
Best Local Similarity:	82.39%	Mismatches:	19
Query Match:	84.49%	Indels:	0
DB:	3	Gaps:	0

US-10-764-259-13 (1-306) x US-09-949-016-590 (1-1541)

Qy	6	AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal	25
Db	46	GAGCTGGACCTGGCTGGAGCAGCTGAACAGAGTGAAGCAGCTGAACGAGAACCAAGTG	105
Qy	26	LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal	45
Db	106	CGGACGCTGTGGAGAGGCAAGGAAATTTTACAAGAGAAATCAAAATGTGCAAGAGGTT	165
Qy	46	LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu	65
Db	166	CGTTGCCCTGTGTACTGTCTGTGGAGATGTCATGGTCAATTTTCATGATCTTATGGAACTC	225
Qy	66	PheArgIleGlyGlyAlaProAspThrAsnTyrIlePheMetGlyAspTyrValAsp	85
Db	226	TTTAGAAATTTGGTGGAAATCACCGGATACAAACTACTTATTTCATGGGTGACTATGTAGAC	285
Qy	86	ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg	105
Db	286	AGAGGATATTATTTCAGTGAGACTGTGACTCTTCTGTAGCATTTAAAGTGGCGTTATCCA	345
Qy	106	AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly	125
Db	346	GAACGCAATTACAAATATTGAGAGGAATCACGAAAGCCGACAAATTACCCCAAGTATATGGC	405
Qy	126	PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp	145
Db	406	TTTTATGATGAATGTCTGCAAGATATGGGAATGCCAACGTTTGGAAATATTTTACAGAT	465
Qy	146	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly	165
Db	466	CTCTTTTGATTATCTTCCACTTACAGCTTTAGTAGATGGACAGATATTTCGCCCTCCAATGGT	525
Qy	166	GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu	185
Db	526	GGCCTCTCTCCATCCATAGACACACTGGATCATATNAGAGCCCTGGATCGTTTACAGGAA	585
Qy	186	ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly	205
Db	586	GTTCACATAGAGGCCCAATGTGTATCTGTATATGGTCAGATCCAGATGATCGTGGTGGG	645
Qy	206	TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe	225
Db	646	TGGGGTATTTCACCACTGGTCTGGCTACACATTTGGACAAGACATTTCTCGAAACCTTT	705
Qy	226	AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr	245
Db	706	ACCATGCCAATGGTCTCACACTGTTTCTCGTGCCACACAGCTTGTATATGGAGGATAC	765
Qy	246	AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg	265
Db	766	AATTGGTGTATGATCGGAATGTGGTATACCATTTTCAGTGCCACCAATTAATCTGTATTCGT	825
Qy	266	CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln	285
Db	826	TGTGGGAACCGAGCTGTATCATGGAATTAGATGACACTTTTAAAAATATTCTCTTCCTCAA	885
Qy	286	PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe	305
Db	886	TTTAGCCCGCGCTCTGTCTGTGAGGCTCATGTTCACGCGCCGACCCACAGACTACTTC	945
Qy	306	Leu 306	
Db	946	CTA 948	

RESULT 8

US-09-780-049-10

```
; Sequence 10, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASES
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASES
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 10
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)...(1125)
US-09-780-049-10

Alignment Scores:
Pred. No.:      4.98e-170      Length:      1781
Score:          1411.00        Matches:    250
Percent Similarity: 93.69%     Conservative: 32
Best Local Similarity: 83.06%   Mismatches: 19
Query Match:      84.49%       Indels:     0
DB:               3           Gaps:        0

US-10-764-259-13 (1-306) x US-09-780-049-10 (1-1781)

Qy      6 AspValAspArgGlnIleGluInLeuSerGluCysLysProLeuSerGly
Db      : ::::: :::::
220 GAGCTGGACCGACTGCATCGAGCAGCTGAACGAGTGCACAGCAGCTCTCCGAA
Qy      26 LysAsnLeuCysAspGlnAlaAraGThrIleLeuValGluGluTrpAsnVal
Db      : ::::: :::::
280 AAGAGCCCCTCGAGAAGGCTAAAGAAATCTGTCAAAAAGAAATCCAAGTT
Qy      46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLei
Db      : ::::: :::::
340 CGATGTCAGTCACTGHTGTGGAGATGTATCGGCCAATTTCATGATCT
Qy      66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAsp
Db      : ::::: :::::
400 TTTAGAATTGCTGTTAAATCACCATACCAATAATACCTGTTTATGGGAGA
Qy      86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa
Db      : ::::: :::::
460 AGAGATATTACTCTGTGTGAACAGTGTACACTGCTTGTTAGTCTCTTAAGTT
Qy      106 AsparGileThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlu
Db      : ::::: :::::
520 GAGCGCATACCATACTCCGAGGGAAATCACGAGAGCAGACAGATCACACA
Qy      126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTy
Db      : ::::: :::::
580 TTCTACACGAGTGTAAAGAAATACGGAATCCAAATGTTTCGAAATAT
Qy      146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys
Db      : ::::: :::::
640 CTTTTTGACTATCTCTCTCTCACTGCCTTGGTGGATGGCAGATCTTCTG
Qy      166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr
Db      : ::::: :::::
700 GGTCTGTCAACATCCATAGACACACTGGATCACATCCGAGCACTCGATCG
Qy      186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAs
Db      : ::::: :::::
760 GTTCTCATGAGGCTCAAATGTGTGACTTGTCTGTGGTCAGATCCAGATGA
Qy      206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAla
Db      : ::::: :::::
820 TGGGGGATATCTCTCGGGAGCTGGTTATACCTTGGCCAAAGATATTTCT
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Alignment Scores:		
Pred. No.:	8.96e-170	Length:
Score:	1411.00	Matches:
Percent Similarity:	92.69%	Mismatches:
Best Local Similarity:	93.39%	Indels:
Query Match:	84.49%	Gaps:
DB:	3	
		2574
		248
		34
		19
		0
		0

US-10-764-259-13 (1-306) x US-09-780-045-3 (1-2574)

Qy	6	AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal	25
Db	1015	GAGCTGGACCAAGTGGGTTCGAGCAGCTGAACGAGTGTAAAGCAGCTGAACGAGAGACCAAGTG	1074
Qy	26	LysAsnLeuCysAspGlnAlaAArgThrIleLeuValGluGluTrpAsnValGlnProVal	45
Db	1075	CGGACGCTGTGCAGAGAAAGGCAAAAGAAATTTTAAACAAAGAAATCAAAATGTGCAAGAGGTT	1134
Qy	46	LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu	65
Db	1135	CGTTCGCTCTGTACTGTCTGTGGAGATGCGATGGTCAATTTATGATGATCTATTGGAACTC	1194
Qy	66	PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp	85
Db	1195	TTTAGAATTGGTGGAAATCACC CGGATACAACTACTTATTCATGGGTGACTATGTAGAC	1254
Qy	86	ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValAArgTyrArg	105
Db	1255	AGAGGATATTATTTCAGTGGAGACTGTGACTCTTCTGTAGCATTTAAAGGTGCGTTATCCA	1314
Qy	106	AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly	125
Db	1315	GAACGCATACAAATATTGAGAGGAATATCAGAAAGCCGACAAATATCCCAAGTATATGGC	1374
Qy	126	PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp	145
Db	1375	TTTTATCATGAATGTCGCGAAAGTAGTGGAAATGCCAACCGTTTGGAAATATTTACAGAT	1434
Qy	146	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly	165
Db	1435	CTCTTTGATTATCTTCCACTTTACAGCTTTTAGTAGAGACAGATATTTCTGCCTCCATGGT	1494
Qy	166	GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu	185
Db	1495	GGCCCTCTCCATCCATAGACACACTGGATCATATAAGAGCCCTGGGATCGTTTACAGAA	1554
Qy	186	ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly	205
Db	1555	GTCCACATCAGGGCCCCAATGTGTGATCTGTATGGTCAGATCCAGATGATCGTGGTGA	1614
Qy	206	TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe	225
Db	1615	TGGGGTATTTCCACCAGCTGGTGTGGGTGCACATTTGGACAAGACATTTCTGTAACACCTTT	1674
Qy	226	AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr	245
Db	1675	AACCATGCCAATGGTCTCACACTGGTTTCTCGTCCCCACACAGCTTGTAATGGAGGGATAC	1734
Qy	246	AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg	265
Db	1735	AAATGGTGTTCATGATCGGAATGTGGTTTACCAATTTTCAGTCACCCCAATTTACTGTTATCGT	1794
Qy	266	CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln	285
Db	1795	TGTGGGAACCAGGCTGTCTATCATCGAATATAGATGACACTTTTAAATAATATTCCTCTTCAA	1854
Qy	286	PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe	305
Db	1855	TTTGACCCAGCCCTCGTGTGGTGGACCTCATGTTACGGCGCACCCACAGACTACTTTC	1914
Qy	306	Leu	306
Db	1915	CTA	1917

RESULT 11
US-09-190-976B-11
; Sequence 11, Application US/09190976B
; Patent No. 6815187
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael

```

1  ;      Horowitz, Arie
2  TITLE OF INVENTION: Stimulation of angiogenesis via
3      syndecan-4 cytoplasmic domain signa
4  ;
5  NUMBER OF SEQUENCES: 25
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: David Prashker, Esq.
8  STREET: P.O. Box 5387
9  CITY: Magnolia
10 STATE: Massachusetts
11 COUNTRY: USA
12 ZIP: 01930
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
16 COMPUTER: Dell PC
17 OPERATING SYSTEM: MS DOS
18 SOFTWARE: Microsoft Word version 97
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/190,976B
21 FILING DATE: 12-No. 6815187-1998
22 CLASSIFICATION: Unknown
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: David Prashker, Esq.
26 REGISTRATION NUMBER: 29,693
27 REFERENCE/DOCKET NUMBER: BIS-041
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (978) 525-3794
30
31 INFORMATION FOR SEQ ID NO: 11:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1721 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37
38 MOLECULE TYPE: peptide
39 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
40 US-09-190-976B-11
41
42 Alignment Scores:
43 Pred. No.: 2 71e-164 Length: 1721
44 Score: 1366.00 Matches: 247
45 Percent Similarity: 92.36% Conservative: 31
46 Best Local Similarity: 82.06% Mismatches: 23
47 Query Match: 81.80% Indels: 1
48 DB: 3 Gaps: 0

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Qy	146	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisIsglulIlePheCysLeuHisGly	165
Db	548	CTTTTGACATATCTCTCTCTCTGCTGGTGGCAGCATCTTCTGTCTACATGGT	607
Qy	166	GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu	185
Db	608	GGCCTCTCCACATCCATAGATACACTGGATCACATCAGAGCACCTTGATCGCCTACAAGAA	667
Qy	186	ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly	205
Db	668	GTTCCCTCATGAGGGTCCAATGTGTGACTTGCTGTGGTCAGATCCAGATGACCCGTGGAGGT	727
Qy	206	TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe	225
Db	728	TGGGGTATATCTCTCCAGGAGCTGGTTACACCTTTGGCCAGGATATTTCTGAGACATTT	787
Qy	226	AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr	245
Db	788	AATCATGCCAATGGCCCTCAGCTTGGTGTCTAGAGCTCATCAGCTGGTGTGATGGAGGGATAT	847
Qy	246	AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTrpCysTyrArg	265
Db	848	AACTGGTGCCATGACCGAATGTAGTAACGATTTTTCAGTGCTCCAAACTATTTGTTATCGT	907
Qy	266	CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln	285
Db	908	TGTGGTAACCAAGTGCAAATCATGGAATCTTGATGATACTCTTAAATACTCTTTCTTCGAG	967
Qy	286	PheGluProAlaProArgGlnSerGluProAspValThrArgIleYsThrProAspTyrPhe	305
Db	968	TTTGACCCAGCACCCCGC-AGAGGGCAGCCACATGTTACTCGTGTGATCCCCAGACTACTTC	1026
Qy	306	Leu 306	
Db	1027	CTG 1029	

RESULT 12

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RS001 12
US-09-487-558B-269
; Sequence 269, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 269
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-269

Alignment Scores:
Pred. No.: 5.53e-155 Length: 1134
Score: 1291.00 Matches: 229
Percent Similarity: 87.67% Conservative: 34

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Best Local Similarity:	76.33%	Mismatches:	37
Query Match:	77.31%	Indels:	0
DB:	3	Gaps:	0
US-10-764-359-13 (1-306) x US-09-487-558B-269 (1-1134)			
Qy	7	ValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLe	ys 26
Db	232	CTTGACCAATGGATTGAGCATTTGAGTAATAATGCGACCATCTATCAGAAGA	CA 291
Qy	27	AsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValG1	ys 46
Db	292	CGACTATGTAATAATGGCGGTGGACGTGTCAGTTCGAGGAGAGATGTTAA	AC 351
Qy	47	CysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeu11	he 66
Db	352	GTGCCTGTTACCAATTTGTGGTGCAGTACACGGTCAATTCATCCATGACTTGT	TC 411
Qy	67	ArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTy	rg 86
Db	412	AAGATTGGTGCTCTGCTCTGCACCAATATACCTTTTCATGGGTGAATP	GA 471
Qy	87	GlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValAr	sp 106
Db	472	GGATATTATTCTGTTGAGACCGTATCTTACTAGTTCCTAGGAAGTCAG	AT 531
Qy	107	ArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnVa	he 126
Db	532	AGAATTACTATACTTAGGGGCAATCACGAGCTAGGCAGAGATTACCCAGT	TT 591
Qy	127	TyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPh	eu 146
Db	592	TATGACCAATGTTTGAGAAAGTAGCGGAGTGCAGAACGTGTGGAAATAGTT	TA 651
Qy	147	PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLe	ly 166
Db	652	TTGATTATTTCGCCGTACTGCGCTTGGTGGATAATAAATCTTCGT	GT 711
Qy	167	LeuSerProSerLeuAspThrLeuAspHisIleAArgAlaLeuAspArg11	al 186
Db	712	CTCTCACCACATGATAGAGACAATAGATCAAGTTAGAGATTTAAATAGAA	TG 771
Qy	187	ProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspAr	rp 206
Db	772	CCTCACAAGAGTCCAATGTGTGACCTTCTATGGTCCGATCCTGATGATAC	GG 831
Qy	207	GlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaG1	sn 226
Db	832	GGATCAGTCCGAGAGTGCAGCGTTCACCTTTGGTCAAGACATCATGTGA	AT 891
Qy	227	HisThrAsnGlyLeuSerLeuValAlaAArgAlaHisGlnLeuValMetG1	sn 246
Db	892	CACACTAATGACCTATCTACTAATAGCAAGAGCTCACCAATTTGGTAAATGGA	CT 951
Qy	247	TrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCy	ys 266
Db	952	TGGTCTCACCAGCAAAATGTTGTACCATTTTTCAGTGCTCCAAATATTTC	GT 1011
Qy	267	GlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPh	he 286
Db	1012	GGTAACCAAGCCCGCTATTATGGAGGTGGATGAAAACCATTAATAGCCAA	AC 1071
Qy	287	GluProAlaProArgGlnSerGluProAspValThrArgLysThrProAs	eu 306
Db	1072	GATCCATCTGTGAGACCGGTGAACCAACCGTCAACAGGAAGACACCGGA	TA 1131

RESULT 13
US-09-614-221A-47
; Sequence 47, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojint
; APPLICANT: Yu, Jaehyuk

Alignment Scores:	
Pred. No.:	5.53e-155
Score:	1291.00
Percent Similarity:	87.67%
Length:	1134
Matches:	229
Conservative:	34

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 DB 508 AGAATTACGATACCTAGAGGCAATCACGAGTCTAGGAGATACCAAGATATACGGGTTT 567
 QY 127 TyrAspGluCysLeuArgIysTyrGlyAenAlaAenValTyrPheThrAspLeu 146
 DB 568 TATGATGAATGTTTGAGAAAGTACGGCAGTGCACAAACGTTGTGAAATGTTACAGATCTT 627
 QY 147 PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGly 166
 DB 628 TTCGATTATTTCCATATACCCGATAGTAGATAATAAATTTCTGCTGTCATGGAGGA 687
 QY 167 LeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluVal 186
 DB 688 CTTTCCCCCATGATAGAACCATATAGATCAGGTGAGAGAGTTGACAGAGATGAGAGT 747
 QY 187 ProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGlyTyr 206
 DB 748 CCTCATGAAGGTCTATGTGTGACCTTCTATGCTCAGACCCCTGACGATAGAGCGGATGG 807
 QY 207 GlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAen 226
 DB 808 GGAATCAGTCCAGAGGTGCGGCTTCACTTTTGACAGAGATGTCAGTGAGCAATTCAAT 867
 QY 227 HisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsn 246
 DB 868 CACACTAATGATCTATCACTAATAGCAGAGCTCACCAATTTGTAATGGAAGGCTATGCT 927
 QY 247 TrpCysGlnAspIleAsnValValThrValPheSerAlaProAsnTyrCysTyrArgCys 266
 DB 928 TGGTCTCACAGCAAAATGTTGTCACCAATTTTCACTGCTCCCTAAATTTACTGCTACAGATGT 987
 QY 267 GlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGlnPhe 286
 DB 988 GGTAAATCAAGCAGCTATCATGAAAGTGGACGAGATCAATAATAGACAATTTCTTACAGTAC 1047
 QY 287 GluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPheLeu 306
 DB 1048 GACCCATCCGTAAAGCAGGTGAACTAGCTGACAGAAAGACCCAGATTTACTTTTAA 1107

RESULT 15

US-09-949-016-2909
 ; Sequence 2909, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2909
 ; LENGTH: 1339
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-2909

Alignment Scores:

Pred. No.: 3,196-135 Length: 1339
 Score: 1137.50 Matches: 204
 Percent Similarity: 81.43% Conservative: 46
 Best Local Similarity: 66.45% Mismatches: 56
 Query Match: 68.11% Indels: 1
 DB: 3 Gaps: 1

US-10-764-259-13 (1-306) x US-09-949-016-2909 (1-1339)
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 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal tp 40
 DB 164 AAGGAGAGCGAAGTCAAGGCCCTGTGCGCTAAGGCCAGAGAGATCTTGGT GC 223
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly is 60
 DB 224 AACGTGCAGAGGGTGGAGCTCGCCAGTCACAGTGTGCGCGGACATCCATG AT 283
 QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr et 80
 DB 284 GACCTCAAGAGCTGTTTCAGAGTAGGTGGCGACGTCCCTGAGACCACTA TG 343
 QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe eu 100
 DB 344 GGGGACTTTGTGGACCGTGGCTTCTATAGCGTCGAAACGTTCCCTCCTGCT TT 403
 QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
 DB 404 AAGGTTGCTATCTGATCGCATCACACTGATCCGGGCAACCATGAGAG TC 463
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 DB 464 ACGGAGGTCTATGGCTTCTACGATGAGTGGCTGGCAAGTACGGCTCGGT GG 523
 QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGly le 160
 DB 524 CGCTACTGCATGAGATCTTTGACTACTCTAGCTGTGTCAGGCATCATCGA TC 583
 QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle eu 180
 DB 584 TTCTGCGTGCACGGGGGCTCTCCCTCCATCCAGACCTGGATCAGAT TC 643
 QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyr ro 200
 DB 644 GACCGAAAGCAAGAGGTGCTCATGATGGGGCCCATGTGTGACCTCCTCTG CA 703
 QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh sp 220
 DB 704 GAAGACACACAGGCTGGGGGTGAGCCCCCGAGGAGCGGCTACCTATT AC 763
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
 DB 764 GTGGTGGGCCAGTTTCAACGCGACCAATGACATTTGACATGATCTGCGGTGC TG 823
 QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPh ro 260
 DB 824 GTGATGGAAGGTTTCAAGTGGCCTTCAATGAGACGGGTGCTCCTGTGTG CC 883
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly sn 280
 DB 884 AACTACTGCTACCGCTGTGGGAATGTGGCACCCATCTTGGAGCTGGACGA AG 943
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa ys 300
 DB 944 AAAGATTTCATCATCTTTGAGGCTGCTCCCAAGACACACGGGGCATCCC AG 1003
 QY 301 ---ThrProAspTyrPheLeu 306
 DB 1004 CCGTGGCCGACTACTTCTCTG 1024

Search completed: December 9, 2005, 12:58:23
 Job time : 212 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:28:16 ; Search time 825 Seconds

(without alignments)
3067.187 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1670	100.0	1365	7	US-10-764-259-8
3	1549	92.8	1386	6	US-10-236-699-21
4	1547	92.6	1330	6	US-10-236-699-31
5	1521	91.1	1243	6	US-10-236-699-7
6	1521	91.1	1525	8	US-10-425-115-160542
7	1518	90.9	1732	7	US-10-425-114-35277

8	1508.5	90.3	1195	7	US-10-437-963-40723	Sequ
9	1508.5	90.3	1298	6	US-10-236-699-25	Sequ
10	1508	90.3	921	3	US-09-938-842A-705	Sequ
11	1508	90.3	921	3	US-09-938-842A-705	Sequ
12	1495	89.5	924	3	US-09-938-842A-571	Sequ
13	1495	89.5	924	3	US-09-938-842A-571	Sequ
14	1478	88.5	1879	8	US-10-425-115-149113	Sequ
15	1456	87.2	1759	8	US-10-425-115-160546	Sequ
16	1456	87.2	1761	7	US-10-424-599-20866	Sequ
17	1452	86.9	1759	7	US-10-425-114-24862	Sequ
18	1431	85.7	1626	7	US-10-425-114-28955	Sequ
19	1431	85.7	1734	8	US-10-425-115-149110	Sequ
20	1429	85.6	1484	8	US-10-739-930-1189	Sequ
21	1427	85.4	1738	6	US-10-388-934-574	Sequ
22	1427	85.4	1787	6	US-10-291-808-39	Sequ
23	1427	85.4	1804	3	US-09-917-800A-1624	Sequ
24	1427	85.4	1804	7	US-10-191-803-83	Sequ
25	1427	85.4	1804	9	US-10-386-971-2	Sequ
26	1427	85.4	2181	6	US-10-007-926A-184	Sequ
27	1427	85.4	2181	7	US-10-467-126-17	Sequ
28	1427	85.4	2181	9	US-10-936-273-20	Sequ
29	1427	85.4	2966	7	US-10-467-126-3	Sequ
30	1411	84.5	1531	6	US-10-210-120-42	Sequ
31	1411	84.5	1531	9	US-10-909-035-42	Sequ
32	1411	84.5	1541	9	US-10-956-157-1198	Sequ
33	1411	84.5	1580	6	US-10-388-934-575	Sequ
34	1411	84.5	1781	7	US-10-467-126-10	Sequ
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38	1411	84.5	1843	7	US-10-467-008-10	Sequ
39	1411	84.5	2574	7	US-10-467-008-3	Sequ
40	1408	84.3	1487	6	US-10-236-699-23	Sequ
41	1408	84.3	1529	3	US-09-880-107-2098	Sequ
42	1404	84.1	1279	6	US-10-236-699-2	Sequ
43	1392	83.4	1263	7	US-10-311-764-14	Sequ
44	1392	83.4	2720	8	US-10-425-115-22335	Sequ
45	1389	83.2	1587	8	US-10-425-115-22332	Sequ

ALIGNMENTS

RESULT 1

US-09-828-302-8
; Sequence 8, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8

Alignment Scores:
Pred. No.: 3.52e-216 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-828-302-8 (1-1365)

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Db ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTGGAGTGCAGCCGTTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
Db TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGAGCATCTTGGTGGAGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db AACGTCGAGCCGTCGAGTGTCTGTACGGTTTCGGGTGACATCCATGGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
Db GATCTCATCGAGCTTTCCGCATAGAGGCAAGGCCCGCCGACACAGAACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
Db GCGCAGCATGTGATCGTGGATATTATTTCTGTCGAGACTGTGTCTCTTAGTGGCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db AAGGTGCGGTATAGGATAGGATCAACATCTTCGAGGGGAACCCAGAGCAGGCAGATT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db ACGCAAGTATATGTTTCTATGATGAATGCTCGGAAGTATGGAAATGCCAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGluHisGluIle 160
Db AAGTACTTTCACGATCTGTTCGACTACCTGCTCTGACAGCTCTCATTCAGCAGCAGATT 550
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db TTTTGTCTTCATGGTGGTGTGCTCTCCATCGCTCGACACATTAGATCATCCGAGCCCTA 610
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTrpSerAspPro 200
Db GATCGTATTCAAGAGTGCAGCAGCGGCGCGATGTGTGATCTACTCTGGTCTGATCCA 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db CATGATCGTTGTGGATGGGCAATTCACACAGGTCGCGGTTACTTTTGGTCAAGAT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db ATTGCAGAGCAGTTCATCATACCAATGGTCTAAGTTTGGTTGACAGTGTCCACCGCTT 790
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValThrValPheSerAlaPro 260
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QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGluThrMetAsn 280
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QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
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RESULT 2

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US-10-764-259-8
; Sequence 8, Application US/10764259
; Publication NO. US20040148658A1
; GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
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; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND M
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/10/764,259
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-764-259-8
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Alignment Scores:
Pred. No.: 3.52e-216 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
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US-10-764-259-13 (1-306) x US-10-764-259-8 (1-1365)

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Db 131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGAGCATCTTGGT 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
Db 191 AACGTGCGGCGGTGAAGTGTCTGTCCGCTTTGGCGGTGACATCCATGG 250
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr 80
Db 251 GATCTCATCGAGCTTTTCCGCATAGAGGCAAGGCCCGCCGACACAGAACTA 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
Db 311 GCGGACTATGTGGATCGTGGATATTATTTCTCGAGACTGTGTGCTCTT 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe 120
Db 371 AAGGTGCGGTATAGGATAGGATCACAACTCTTCGAGGGGAACCCAGAGAG 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
Db 431 ACGCAAGTATATGTTTCTATGATGAATGCCCTCGGAAGTATGGAATGCT 490
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGln 160
Db 491 AAGTACTTTCACGATCTGTTCGACTACCTGCTCTGACAGCTCTCATTCAG 550
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
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QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTrp 200
Db 611 GATCGTATTCAAGAGTGCAGCAGCGGCGCGATGTGTGATCTACTCTGGTCT 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGly 220
Db 671 CATGATCGTTGTGGATGGGCAATTCACACAGGTCGCGGTTACTTTTGGTCA 240
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla 260
Db 731 ATTGCAGAGCAGTTCATCATACCAATGGTCTAAGTTTGGTTGACAGTGTCC 280
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValThrValPheSerAla 300
Db 791 GTGATGGGAAGGATACAATTTGGTGCAGGATAAAATGTTGTCCAGTTCAGT 306
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGluThrMet 320
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RESULT 2

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; Sequence 8, Application US/10764259
; Publication NO. US20040148658A1
; GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
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Qy 301 ThrProAspTyrPheLeu 306
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; Sequence 21, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Glycine max
US-10-236-699-21
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Score: 1549.00 Matches: 280
Percent Similarity: 96.73% Conservative: 16
Best Local Similarity: 91.50% Mismatches: 10
Query Match: 92.75% Indels: 0
DB: 6 Gaps: 0
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Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
Db 152 TCGGAGTCGGAGTGTAAGCGCTGTGCGATCAAGCGGAGCAGCATTTCTTGTGGAGGAGTGG 211
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 212 AACGTGCAACCGTTTAAGTCCCGCTGACCGCTGCGGCGATATTCAGCGCAGTCTAC 271
Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
Db 272 GATCTCATGAGCTGTTTCGGATTGGAGGAGCGCTCCCGATACCAATATCTCTTCATG 331
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
Db 332 GGTGATTATGATAGCTGGGATCTATTTCAGTGGAGACTGTTACACTTTTGTGGCTTTG 391

Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer 120
Db 392 AAGATCCCTTTATAGAGATAGAAATCAATTTCTCAGGGGAAATCATGAAG 451
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 140
Db 452 ACTCAAGTGTATGGCTTCTATGATGAATGCTTGAGAAAAATATGGAATGC 511
Qy 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleG 160
Db 512 AAATACITTTACAGACTTCTTTGATTTATTTGCTCTGACTGCCCTCATTTGA 571
Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI 180
Db 572 TTCGCTTGCATGGAGGTCTCTCACCTTCTTTGGATACACTGGATAACA 631
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr 200
Db 632 GATCGTATTCAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTGTG 691
Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh 220
Db 692 GATGATCGCTGTGGATGGGGAATATCTCCACGTGGTGCAGGATACACAT 751
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240
Db 752 ATAGCTGCTCAGTTTAAATCATACCAATGGCTCTCTCCCTGATATCGAGAC 811
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh 260
Db 812 GTTATGGAAGGATTCAATTTGGTGGCAGGACAAAGAAATGTGGTACTGTATT 871
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG 280
Db 872 AATTACTGTTATCGATGTGGGAATATGGCTCCCATACTAGAAATAGGAGA 931
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa 300
Db 932 CAGAATTTCTTCAGTTTGATCCAGCTCCAGGCAAAATTTGAGCCTGACAC 991
Qy 301 ThrProAspTyrPheLeu 306
Db 992 ACTCCAGATTATTTTGT 1009
RESULT 4
US-10-236-699-31
; Sequence 31, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-31
Alignment Scores:
Pred. No.: 1,95e-199 Length: 1330
Score: 1547.00 Matches: 280

Percent Similarity: 96.41% Conservative: 15
Best Local Similarity: 91.50% Mismatches: 11
Query Match: 92.63% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-236-699-31 (1-1330)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysIysProLeu 20
DB 104 ATGCGGTCTCACGCGATCTGGAACGACAGATCGAGCAGCTGATGGAGTCAAGCCTCTG 163
QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleSerLeuValGluLysTrp 40
DB 164 TCGGAGTCGGAGGTGAAGCGCTGTGTATCAAGCGAGGCGCATTTCTCGTGAGGAATGG 223
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 224 AACGTGCAACCGTGAAGTGGCCCGTCAACCGTCTGCGGCGATATTCACGGCCAGTTTAC 283
QY 61 AspLeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsnTyrIleuPheMet 80
DB 284 GATCTCATCGAGCTGTTTCGGATTGGAGGGAACGCCCGCATACCAATATCTCTTCATG 343
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 344 GGTGATTATGTAGATCGTGATCTATTTCAGTGGAGACTGTTTACACTTTTGTGGCTTTG 403
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 404 AAGTCCGTTACAGAGATAGATCAATCTTCAGGGGAATCATGAAGTCGTCAAT 463
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 464 ACTCAAGTGTATGGCTTCTATCATGAATGCTTGAGAAAATATGGAATGCCAATCTCTGG 523
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 524 AAATACTTTACAGACTGTGTTGATTATTTACCTCTGACTGCCCTCATTTGAGAGTCAGATT 583
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 584 TTCCTGTCATGGAGGCTCTCACCTCTTTGGATACACTGGATAACATCAGACATTG 643
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 644 GATCGTATACAAGAGGTTCCATCAATGAAGGACCAATGTGTGATCTCTGTGTCTGACCT 703
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 704 GATGATCGCTGTGGATGGGAATATCTCCACGTGTGCAGGATACACATTTGGACAGGAT 763
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 764 ATAGCTGCTCAGTTTAATCATACCAATGCTCTCCCTGATATCAGAGCTCATCAGCTT 823
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspIysAsnValThrValPheSerAlaPro 260
DB 824 GTTATGAAGGATTCAAATTTGGTCCAGGACAAAATGTGGTCACTGTATTTAGTGCACCA 883
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
DB 884 AATTACTGTTACCGATGTGGGAATATGGCTGTATCTACTAGAATATGGAGGAATATGGAT 943
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
DB 944 CAGAAATTTCTTCAGTTTGATCCAGCGGCCAGGCAAAATTTGACCTTGACACACAGCGAAG 1003
QY 301 ThrProAspTyrPheLeu 306
DB 1004 ACTCCAGATTAATTTT 1021
```

RESULT 5

US-10-236-699-7

; Sequence 7, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEP
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-236-699-7

Alignment Scores:
Pred. No.: 6,11e-196 Length: 1243
Score: 1521.00 Matches: 272
Percent Similarity: 95.42% Conservative: 20
Best Local Similarity: 88.89% Mismatches: 14
Query Match: 91.08% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-236-699-7 (1-1243)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysIys 20
DB 150 ATGCGGAGAGCGGAGACATCGATCGTCAGATCGAGCAGCTGATGGAGTGT 209
QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
DB 210 TCCGAGGCGGAGGTCAAGACGCTGTGCGAGCAAGCGAGGCGGATTTCTGGT 269
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGly 60
DB 270 AATGTTACGCGGTAAAGTGTCCGCTCACCTGTGCGGCGACATCCACGG 329
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr 80
DB 330 GATCTGATTGAGCTTTTAAAGATCGGTGTTCTTCGCTGACACCAATTA 389
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 390 GCGGATTACGTAGATCGAGGTTATTTCTGTGGAGACAGTCTCGCTCTT 449
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120
DB 450 AAAGTTCGCTACAGATAGGCTTACCATCTTAAGAGGGAATCAGAAAG 509
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
DB 510 ACTCAAGTGTATGGATTTTATGATGAGTGTCTTGAGAAAATATGGAATGC 569
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGlu 160
DB 570 AAACACTTCACTGACCTTTTGTATTTCTCTCTTACAGCTCTCATCGA 629
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
DB 630 TTCTGTTTACATGAGGCTCTCACCTTCTTTAGATACACTTGACACAT 689
QY 181 AspArgIleGlnGluValProHisGlyGlyProMetCysAspLeuLeuTrp 200
DB 690 GATCGAATCCAAAGAGTTCCACATGAAGGACCTATGTGTGATCTGTTATGC 749
```

201	AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp	220
750	GATGATCGATCGCGGTGGGGAATATCTCTCGTGGCGAGGCTACAGTTGGGACAGAT	809
221	IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu	240
810	ATCGCTACTCAGTTTAACCAACCAATGGACTCAGTCTGATCTCAAGAGCACACCAACTT	869
241	ValMetGluGlyTyrAsnTrpCysGlnAspIleAsnValValThrValPheSerAlaPro	260
870	GTCAATGGAAGTTATAATTGGTGCCAAAGAAGACGTTGTGACTGTGTTTAGCGCCCA	929
261	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn	280
930	AACATTATGCTACCGATCGCGCAACATCGCTGCTATTCTAGAGATAGACGAGAAATGGAC	989
281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgGly	300
990	CAGACCTTCCTTCAGTTTCGATCCAGCCCAAGCTCAGTAGAACCCGAACTACACGGAAA	1049
301	ThrProAspTyrPheLeu	306
1050	ACTCCAGATTACTTTTGTG	1067

RESULT 6

```

US-10-425-115-160542
; Sequence 160542, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160542
; LENGTH: 1525
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(1525)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_77994C.1
US-10-425-115-160542

```

Alignment Scores:

Pred. No.:	8.43e-196	Length:	1525
Score:	1521.00	Matches:	272
Percent Similarity:	96.41%	Conservative:	23
Best Local Similarity:	88.89%	Mismatches:	11
Query Match:	91.08%	Indels:	0
DB:	8	Gaps:	0

US-10-764-259-13 (1-306) x US-10-425-115-160542 (1-1525)

Qy	1	MetProSerTyrAlaAspValaAspValaAspGlnIleGluInLeuSerGluCysIysProLeu	20
Db	246	ATGCCATCGACGGGATCTGGACCGCCAGATCTCGCAGCTCGGGATTCCAAGTTCCCTG	305
Qy	21	SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleuValGluGluTrp	40
Db	306	CCTGAGCGGAGGTCAAACGCTATGCGAGCGCAAGCGCATCTCATGGAGGATGG	365
Qy	41	AnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis	60
Db	366	AACTGTGCAGCCGTCGGCTGCGCCGTCACCTCTCTGGCGGCACATCATCGCCGCACTTCAC	425

Qy	61	AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer	201	AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh	301	ThrProAspTyrPheLeu 306	
Db	426	GACCTCATCGAGCTCTTTTCGCATCGTGGCGACGCGCCGACCAACTTA	546	AAAGTACGTTATAGAGACAGAATCACAAATATTGAGAGGAAATCATGAGAG	846	GATGACAGATGTGGATGGGAAATTTCCAAAGGGTGTCTGGATACACATT	1146	ACCCGACACTTTTGG 1163	
Qy	81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu	121	ThrGlnValTyrGlyPheTyrAspGluCysLeuargLysTyrGlyAsnAl	221	IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl	Qy	281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa
Db	486	GGCGACTACGTCGACCGTGGCTATTACTCACTGGAGACTGTGTCTTATT	606	ACTCAAGTGTATGCGCTTCTATGATGAATGCTTGGCGAAATATGGAAATGCG	906	ATTGCACAACAATTCACCATACAAATGGGCTAAGTCTTATTTCAGAGC	Db	1086	CAGNACTTCCTCAATTCGACCCAGCTCCGCGGCAGATTGAGCCGCAAT
Qy	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer	141	LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG	241	ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh	Qy	261	AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGl
Db	546	AAAGTACGTTATAGAGACAGAATCACAAATATTGAGAGGAAATCATGAGAG	666	AAGTACCTTTACAGACTTGTTTGATTATTTTGGCTCTCAGAGCTCTTATAGA	966	GTAATGGAAGGGTTCATTTGGTGCAGGATAAGAACGTTGTGACAGTGT	Db	1026	AACATTATGCTACCGATCGGGAAATGCGCTCGATCTCTCGAAATTTGGCGA
Qy	161	PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisAl	181	AspArgIleGlnGluValProHisIleGluGlyProMetCysAspLeuLeuTr	281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa	Qy	301	ThrProAspTyrPheLeu 306
Db	726	TTCTGCGCTACATGCTGGTCTCTCTCCATCACTGGATACCTTTGGATAATGT	786	GATCGCATACAAGAGGTCCCGCATGAAGGACCTATGTGTGATCTTTTGTGC	1086	CAGNACTTCCTCAATTCGACCCAGCTCCGCGGCAGATTGAGCCGCAAT	Db	1146	ACCCGACACTTTTGG 1163

RESULT 7

```

US-10-425-114-35277
; Sequence 35277, Application US/10425114
; Publication No. US20040034888A1
;
GENERAL INFORMATION:
;
; APPLICANT: Liu, Jingdong
;
; APPLICANT: Zhou, Yihua
;
; APPLICANT: Kovalic, David K.
;
; APPLICANT: Screen, Steven E
;
; APPLICANT: Tabaska, Jack E
;
; APPLICANT: Cao, Yongwei
;
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
;
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improv
;
; FILE REFERENCE: 38-21(53313)B
;
; CURRENT APPLICATION NUMBER: US/10/425,114
;
; CURRENT FILING DATE: 2003-04-28
;
; NUMBER OF SEQ ID NOS: 73128
;
; SEQ ID NO 35277
;
; LENGTH: 1732
;
; TYPE: DNA
;
; ORGANISM: Zea mays subsp. mexicana

```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE90H04_FLI
US-10-425-114-35277

```

Alignment Scores:	
Pred. No.:	2.64e-195
Score:	1518.00
Length:	1732
Percent Similarity:	86.41%
Conservative:	23
Best Local Similarity:	88.89%
Mismatches:	11
Query Match:	90.90%
Indels:	0
DB:	7
Gaps:	0

US-10-764-259-13 (1-306) x US-10-425-114-35277 (1-1732)

Qy	1	MetProSerTyrAlaAspValAspArgGlnIleGluGlnIleuSerGluCysLysProLeu	20
Db	222	ATCCGTCGACCGGGATCTGGACCAACAGATCTCGCAGATTCGCGGATTCGAAGTTCCTG	281
Qy	21	SerGluLeuGluValLysAsnLeuCysAspAlaAArgThrIleLeuValGluGluTyr	40
Db	282	CCGAGGTGGAGGTCAAGACGCTATGGAGAGGCAAGGCGATCTCTATGGAGGAGTGG	341
Qy	41	AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis	60
Db	342	AACGTACAGCCCGTCGCTCCCGTCACTGTGTGCGCGACATCCACGCCAGTTCCTAC	401
Qy	61	AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMet	80
Db	402	GACCTCATCAGCTCTTCGCGATCGCGGGCGACGCCGACACCACTACCTCTTTATG	461
Qy	81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu	100
Db	462	GGCGATTACGTCGACCGTGGCTACTCTCTGTGGAGACTGTGTCTGTTGTAGTGGCTCTA	521
Qy	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle	120
Db	522	AAAGTACGTTATAGAGACAGAATCACAAATATTGAGAGAGAAATCATGAGAGCAGACAATA	581
Qy	121	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyr	140
Db	582	ACTCAAGTGATGGCTTCTATGATGAATGCTTCGGAAATATGGAATGCAATGTGTGG	641
Qy	141	LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle	160
Db	642	AAGTACTTTACAGACTTGTGTTGATTATTTGGCTCTCAAGCTCTATAGAAAACCAAGATC	701
Qy	161	PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu	180
Db	702	TTCTGCCCTACATGGTGTGTCTCTCCATCATCTGGATACATTGGATAATATCCCGCGCCTT	761
Qy	181	AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyrSerAspPro	200
Db	762	GATCGCATACAGAGGTCCACATGAGGACCTATGTGTGATCTTTTGGTCTGACCCA	821
Qy	201	AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp	220
Db	822	GATGACCGATGTGGGTGGGAAATTTCACCAAGGGGTGTGGATACACATTTGGCGCAAGAT	881
Qy	221	IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu	240
Db	882	ATTGCACACAAATTCACCATACAAATGGGCTTAAGTCTTATTTCAAGGCGACATCAACTT	941
Qy	241	ValMetGluGlyTyrAsnTyrPheGlnAspLysAsnValValThrValPheSerAlaPro	260
Db	942	GTAATGAAGGCTTCAATTGGTGTGAGATAAAGAAATGTGTGACTGTGTTCAGCGCGCT	1001
Qy	261	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn	280
Db	1002	AATCTACTGCTACCGATCGGAAAATGCTGCAATCTCTCGAAATTTGGCGAGAAATGATG	1061
Qy	281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys	300
Db	1062	CAGAAATTCCTTCCAAATTCGACCCAGCTCCACGGCAAAATTGAGCCGATCAGCCGCAAG	1121

Qy 301 ThrProAspTyrPheLeu 306
|||
p/p 1122 ACACCAGACTACTTTTGT 1139

RESULT 8

```

US-10-437-963-40723
; Sequence 40723, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Mol
; FILE NO OF INVENTION: Plants and Uses Ther
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 40723
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT4530
US-10-437-963-40723

```

	Pred. No.: 2.9e-194	Length:	1195
	Score: 1508.50	Matches:	272
	Percent Similarity: 66.0%	Conservative:	23
	Best Local Similarity: 88.60%	Mismatches:	11
	Query Match: 90.33%	Indels:	1
	DG: 7	Gaps:	1
Alignment Scores:			

US-10-764-259-13 (1-306) x US-10-437-963-40723 (1-1195)

Qy	1	MetPro---SerTyrAlaAspValAspArgGlnIleGluInLeuSerGln	19	co
Db	1	ATGCCGTCGTCGACGGGGATCTGCACGGCAGATCGCGAGCTCGCGGA	60	AC
Qy	20	LeuSerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleLeu	39	lu
Db	61	CTGGCGGAGGGGAGGTGAGGGCGCTGTGCAGCAGCGGAAGGCCATCCT	120	AG
Qy	40	TrpAsnValGlnProValIysCysProValThrValCysGlyAspIleHis	59	ie
Db	121	TGGAACGTGCAGCGGTGCGTCCCGTCAAGGCTCTGCGCGCATCCAA	180	TC
Qy	60	HisAspLeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsi	79	ie
Db	181	TACGACCTCATCGAGCTCTTCGCATCGCGCGCGAGCGCCCGACACAA	240	TC
Qy	80	MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeu	99	la
Db	241	ATGGCGCACTAGCTGCACGGTGGCTACTCTCAGTGGAGACTGTTTGGTT	300	TT
Qy	100	LeuIysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGln	119	ln
Db	301	TTCAAAAGTAGCTACAGAGATCGAATTACAATATTGAGAGGAATCATGA	360	TA
Qy	120	IleThrGlnValTyrGlyPheTyrAspGluCysLeuArgIysTyrGlyAsi	139	al
Db	361	ATCACCTCAAGTGTACGGCTTCTACGATGAATGCTTTGAGAAAGTAGTGA	420	TA
Qy	140	TrpIysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIle	159	lu
Db	421	TGCAATACTTTACAGACTGTTTTCATTTATTTGCTCTTCACAGCTCTATT	480	AG

Qy	160	IlePheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAla	179
Db	481	GTGTTCCTGCCTTCACGGTGGCTCTCTCCATCATGTGGATACTTTAGATAACATCCGTGCT	540
Qy	180	LeuAspAtrqIleGlnGluValProHisgluGlyProMetCysAspLeuLeuTyrSerAsp	199
Db	541	CTTGATCGTATACAGAGGTTCCCTCATGAGAGACCCATGTGTATCTTTTGTGGTCTGAC	600
Qy	200	ProAspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGln	219
Db	601	CCAGATGACAGATGCGCGTGGGGAATTTCCAGAGAGCAGCGTTATACATTTGGGCAA	660
Qy	220	AspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGln	239
Db	661	GATATCGCTCAACAGTTTAAACATACAATGGTCTATCTCTCATCAAGGGCACATCAA	720
Qy	240	LeuValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAla	259
Db	721	CTTGTAATGGAAGGATTTAATTTGGTGTGAGACACAAGAATGTTGTGACGGTCTTCAGTGCA	780
Qy	260	ProAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMet	279
Db	781	CCAAACTACTGTATTCGTGTGGTAACAATGCTGCAATTTCTGAGATTTGGCGAAAAATG	840
Qy	280	AsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArg	299
Db	841	GATCAGAACTTCCTCCATNTTGTATCCAGCTCTCTGGCAATTTGAACCAAGACACAAACAGC	900
Qy	300	LysThrProAspTyrPheLeu	306
Db	901	AAGACTCCCGACTACTTTTGTG	921

RESULT 9

```

US-10-236-699-25
; Sequence 25, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1298
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-25

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Alignment Scores:		
Pred. No.:	3.3e-194	Length:
Score:	1508.50	Matches:
Percent Similarity:	66.09%	Conservative:
Best Local Similarity:	88.60%	Mismatches:
Query Match:	90.33%	Indels:
DB:	6	Gaps:
		1
		1
		1598
		272
		23
		11
		1

US-10-764-259-13 (1-306) x US-10-236-699-25 (1-1298)

QY 1 MetPro---SerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysPro 19
||||| :|||:: |||:||||| ||||| ||||| ||||| |||||
Db 173 ATGGCGTCGTCTGCACGGGGATCTGCGCGGAGATCGGCAGCTCGGGAGTGCAAGCAC 232

QY 20 LeuSerGluLeuGluValLysAsnLeuCysAspGlnAlaAraThrIleLeuValGluGlu 39

[illegible]

RESULT 10
115 00 028 0423 705

US-09-938-842A-705
: Sequence 705. Application US/09938842A

; sequence 703, Application
; Patent No.: US20020160378A1

GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun

APPLICANT: wang, xuh
APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS

; TITLE OF INVENTION: SAME

```

; FILE REFERENCE: SCRIPI300
: CURRENT APPLICATION NUMBER

```

;
: CURRENT APPLICATION NUMBER: 200

;
CURRENT FILING DATE: 200

•

r.

TS CONTAINING

```
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 705
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-705
```

```
Alignment Scores:
Pred. No.: 2,256-194 Length: 921
Score: 1508.00 Matches: 272
Percent Similarity: 94.44% Conservativeness: 17
Best Local Similarity: 88.89% Mismatches: 17
Query Match: 90.30% Indels: 0
Gaps: 3
```

US-10-764-259-13 (1-306) x US-09-938-842A-705 (1-921)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGAAGCCGTTA 60
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
DB 61 GGTGAAGCAGACGTCAGAGATCCTTTGGCATCAAGCTAAAGCGATTCTTTGAGGAAT 120
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATCGCGCATCATCATGGCCAGTTTAT 180
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
DB 181 GACCTAAATTGAGCTATTTCGTAATGGTGAATGCTCTGTGATCTAATACCTCTCTCATG 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 241 CGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTATTGGTGGCAITTA 300
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 301 AAGGTGCGTTACAGGACAGACTTACGATCTCTCGCAGGGAATCATGAGAGCCGTCAGATT 360
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 361 ACACAACTATGTTTTTATGACGAATGCTTGAGGAATACGGAATGCAAAATGTGTGG 420
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 421 AAGTATTTTACGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGATCAGGTT 480
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 481 TTCTGTGTTCATGAGAGCCCTTTACCTCTCTCTGGATCTCTTGAACAATATCCGAAGCTTG 540
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 541 GATCGAATACAGAGGTTCCACAGAGGACCAATGTGGCATCTACTCTGGTCTGATCCC 600
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 601 GACGATCGTTGTGGATGGGAATATCTCTCTGTGTGTGGTTACAGCTTTTCGACAGGAC 660
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 661 ATTGCTACTCAGTTTAAATCAATACCAATGGACTGAGTCTGATCTCAAGAGCGCATCACTT 720
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
```

```
DB 721 GTAATGGAGGCTATATTTGGTGTCTAGGAAAGACGTAGTCACAGTGT 780
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly 280
DB 781 AACTACTGTTACAGATGTGGAACATGCGCCCAATTTCTTGAGATTGGAGAJ 840
QY 281 ArgSerPheLeuGlnPheGluProAlaProAlaProArgGlnSerGluProAspVal 300
DB 841 CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAGTCGAACCCGATAC 900
QY 301 ThrProAspTyrPheLeu 306
DB 901 ACCCTGATTAATTTTTTG 918
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RESULT 11

US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Publication No. US20040009476A9

; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC
; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIP1300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 705

; LENGTH: 921

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-705

Alignment Scores:
Pred. No.: 2,256-194 Length: 921
Score: 1508.00 Matches: 272
Percent Similarity: 94.44% Conservativeness: 17
Best Local Similarity: 88.89% Mismatches: 17
Query Match: 90.30% Indels: 0
Gaps: 3

US-10-764-259-13 (1-306) x US-09-938-842A-705 (1-921)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys 20
DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGT 60
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
DB 61 GGTGAAGCAGACGTCAGAGATCCTTTGGCATCAAGCTAAAGCGATTCTTTGT 120
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATCGCGCATATCCATGGA 180
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr 80
DB 181 GACCTAAATTGAGCTATTTCGTAATGGTGAATGCTCTGTGATCTAATACCT 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 241 GGAGATTATGTAGATCGGTGCTACTATTCTGTAGAAACAGTCTCTCTATT 300
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120
```

Db 301 AAGTGGCGTTACAGGACAGACACTTACGATCCTCGAGGGAATCATGAGAGCCGTCAGATT 360
Qy 121 ThrGlnValTyrGlyPheTyrAspGlyCysLeuArgLysTyrGlyAsnAlaSerValTrp 140
Db 361 ACACAGTCTATGGTTTATGACGAATGCTTGAGAAATACGGAATGCAAAATGTGTGG 420
Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuLeuHisGluLe 160
Db 421 AAGTATTTACGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGATCAGGTT 480
Qy 161 PheCysLeuHisGlyCysLeuSerProSerLeuAspThrLeuAspHisLeArgAlaLeu 180
Db 481 TTCTGTTCATGAGGCGCTTTCACCTTCTCTGGAATCTCTTTCGACAAATATCCGAGCTTG 540
Qy 181 AspArgGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 541 GATCGAATACAGAGGTTCCACAGAGGACCAATGTGGATCTACTCTGCTGATCCC 600
Qy 201 AspAspArgCysGlyTrpGlyLeuSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 601 GACGATCGTTGGATGGGAATATCTCTCTGCTGGTGTGCTTACACGTTTGACAGGAC 660
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 661 ATTGCTACTCAGTTAATCATAAACAATGGAGCTGAGTCTGATCTCAAGAGCGCATCAACTT 720
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 721 GTAATGGAGGCTTAATTTGGTGTGAGGAAGACGTAGTACAGTGTTTAGTGACCG 780
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsn 280
Db 781 AACTACTGTTACAGATGTGGAAACATGCGCGCAATCTCTTGAGATTGGAGAAAGATGGA 840
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 841 CAGAACTTCTCTCAATTCGATCCAGACCCCTAGACAAAGTCGAACCGGATACCGGCAAG 900
Qy 301 ThrProAspTyrPheLeu 306
Db 901 ACCCTGATATTTTGG 918

RESULT 12
US-09-938-842A-571
; Sequence 571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

Alignment Scores:
Pred. No.: 1.34e-192 Length: 924
Score: 1495.00 Matches: 268
Percent Similarity: 95.41% Conservative: 23

Best Local Similarity: 87.87% Mismatches: 14
Query Match: 89.52% Indels: 0
Db: 3 Gaps: 0
US-10-764-259-13 (1-306) x US-09-938-842A-571 (1-924)
Qy 2 ProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysGly 21
Db 7 CGCGGACCGGAGATATCGATCGTCAGATCGAGCAGCTTATGGAGGTAA 66
Qy 22 GluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValG 41
Db 67 GAAACGGAGGTGAAGATGTTGTGTGAGCACCAAGACGATTTCTTTGTGGA 126
Qy 42 ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyG 61
Db 127 GTTCAACCGGTTAATGTCCGGTTACCGTCTGCGGTGATATCCACGGCA 186
Qy 62 LeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLe 81
Db 187 CTAATCGAGCTTTTTCGTATCGTGGTGTCTCTCTGATACTAATATCT 246
Qy 82 AspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuVa 101
Db 247 GATTATGTTGATCGAGGGTATTATTCTGTGAGACAGTCTCACCTTTTGGT 306
Qy 102 ValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerAr 121
Db 307 GTTGTGACAGATAGACTTACTATCTTAAGAGGGAATCATGAAGCCG 366
Qy 122 GlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAs 141
Db 367 CAAGTGTATGGTTTTATGATGAATGTTTGGAGAAATATGAAATGTAA 426
Qy 142 TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHi 161
Db 427 CACTTCACTGATCTTTTGTGATTTCTTCCACTTACAGCTCTTATTGAGAG 486
Qy 162 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleAr 181
Db 487 TGTTTACATGAGGACTTTTACCTTCTTTAGATACACTTGACATCCG 546
Qy 182 ArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSe 201
Db 547 CGAATTCAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTATGTC 606
Qy 202 AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGl 221
Db 607 GACCGATCGGTTGGGAAATATCTCTCGTGTGCGAGCTACACTTTCCG 666
Qy 222 AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHi 241
Db 667 GCTACTCAGTTTACCAACCAATGGACTCTCTCTGATTTCAAGAGCACA 726
Qy 242 MetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSe 261
Db 727 ATGGAAGGTTTAAATGCTGCGCAAGAAAGACGTTGTGACTGTATTAG 786
Qy 262 TyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluTh 281
Db 787 TATTGCTACCGTTGTGGCAACATGCTCGCATTTCTAGAGATCGGTGAGAA 846
Qy 282 SerPheLeuGlnPheGluProAlaProAspGlnSerGluProAspValTh 301
Db 847 AATTTCCTTCAAGTTGATCCAGCTCCAGTCAAGTTCGAACCCGAAACCA 906
Qy 302 ProAspTyrPheLeu 306
Db 907 CCAGATTATTTTGG 921

RESULT 13
US-09-938-842A-571
; Sequence 571, Application US/09938842A

```
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

Alignment Scores:
Pred. No.: 1.34e-192 Length: 924
Score: 1495.00 Matches: 268
Percent Similarity: 95.41% Conservative: 23
Best Local Similarity: 87.8% Mismatches: 14
Query Match: 89.5% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-938-842A-571 (1-924)

Qy 2 ProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysLeuProLeuSer 21
Db 7 CCGGCGACGGAGATCGATCGTCAGATCGAGCGAGCTTATGGATGTAAAGCGTTACT 66

Qy 22 GluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluIleTrpAsn 41
Db 67 GAAACGGAGGTGAAGATGTTGTGAGCAGCGCAAGACGATCTTGTGGAAGAGTATAAT 126

Qy 42 ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyClnPheHisasp 61
Db 127 GTTCAACCGGTAAATGTCCGGTTACCGTCTCGGTGATATCCACGGCAATTTTACGAT 186

Qy 62 LeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMetGly 81
Db 187 CTAAATCGAGCTTTTCGTATCGGTGGTCTCTCTGATCTAAATATCTTTTCATGGGT 246

Qy 82 AspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLys 101
Db 247 GATTATGTTGATCGAGGGTATTATTCTGTGGAGACAGTCTCACTTTTGTAGCACTGAAA 306

Qy 102 ValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThr 121
Db 307 GTTCGTTACAGAGATAGACTTACTATCTTAAGAGGAATCATGAAGCGGTCAAAATTACT 366

Qy 122 GlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLys 141
Db 367 CNAAGTGTATGGTTTATGATGAATGTTTGAGAAATATGGAATGCTAAATGTATGGAG 426

Qy 142 TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePhe 161
Db 427 CACTTCACTGATCTTTTGAATATCTTCCACTTACAGTCTTATTGAGAGTCAAGTTC 486

Qy 162 CysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAsp 181
Db 487 TGTTTACATGGAGGACTTTTCACTCTTTTATGATACACTTGACAACATCCGATCTTTAGAT 546

Qy 182 ArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAsp 201
Db 547 CGAATTCAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTATGTTGATCCAGAT 606
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```
Qy 202 AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlu 221
Db 607 GACCGATCGGTTGGGAATATCTCTCGTGGTCAGGCTACACTTTCGG 666

Qy 222 AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHis 241
Db 667 GCTACTCAGTTTAAACCAACACCAATGGACTCTCTCTGATTTCAAGAGCACA 726

Qy 242 MetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSer 261
Db 727 ATGGAAGTTTAAATGGTCCCAAGAAAAGAACGTTGTGACTGTATTTAG 786

Qy 262 TyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThr 281
Db 787 TATTGCTACCGTTTGTGGCAACATGGCTCGCATTTCTAGAGATCGGTGAGAA 846

Qy 282 SerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThr 301
Db 847 AATTTCCTTCAGTTTGATCCAGTCCAGTCCAGTCAAGTCGAACCCGAAACCA 906

Qy 302 ProAspTyrPheLeu 306
Db 907 CCAGATTATTTTGG 921

RESULT 14
US-10-425-115-149113
; Sequence 149113, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 149113
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_67515C.1
US-10-425-115-149113

Alignment Scores:
Pred. No.: 8.47e-190 Length: 1879
Score: 1478.00 Matches: 268
Percent Similarity: 94.81% Conservative: 24
Best Local Similarity: 87.01% Mismatches: 14
Query Match: 88.50% Indels: 2
DB: 8 Gaps: 0

US-10-764-259-13 (1-306) x US-10-425-115-149113 (1-1879)

Qy 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCyl 20
Db 192 ATGCGTTCGACGGGGATCTGACCGGCAGATCGCGAGCTGCGGCGACTG 251

Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
Db 252 CCCGAGGCGGAGGTCAAGGCGCTCTGCGAGCAGGCCAAGGCCATCCTTAT 311

Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlu 60
Db 312 AACGTGACGCCCGTCGCTGCCCTCCCTGTCACCGTCTCGCGCGCATCCACGG 371

Qy 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyr 80
Db 372 GACCTCATCGAGCTCTTCCGCATCGGCGGCGACTCTCCCGACACCAACTA 431
```

```
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
Db 432 GCGACTAGTGCATCGTGGCTATTATTCAGTTGAACAGTTTCTGTAGTGGCTTG 491
QY 101 LysValArgTyrArgAspArgIleThrLeuLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 492 AAAGTCCGTTACAGAGATAGATTACAATACATTAGAGGAAATCATGAGACAGACAAATC 551
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaValTrp 140
Db 552 ACTCAAGTATATGGCTTCTATGATGAATGCTTATAGAAAATATGGAATATGCAATGTCTGG 611
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db 612 AAGTATTTTACAGACTGTGTTGATTTTGGCTCTCACAGCTCTTATAGAAAATCAGGTG 671
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleAlaGlnLeu 180
Db 672 TTCTGTCTTTCATGGTGGCTCTCTCCGTCATTGGACACATTGGATAATATTCGTTCTCTT 731
QY 181 AspArgIleGlnGluValPro-HisGluGlyProMetCysAspLeuLeuTrpSerAspPr 200
Db 732 GATCCGTACAGAGGTTCTCCATGAAGGACCCATGTGTGATCTTTTGTGTCTGACCC 791
QY 200 oAspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAs 220
Db 792 AGATGACCGATGTGGATGGGAATTTCCACGAAGAGAGAGAGGTTACACATTTGGGCAAGA 851
QY 220 PileAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLe 240
Db 852 CATTCGCGAGCAGTGTCAACCATACAAATAGTCTTTCTCTCATTTTCAAGGCGCCATCAACT 911
QY 240 uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPr 260
Db 912 TGTAAATGAAGAATTAATATGGTCCAGATGAAGAATATGATGACAGTCTTCAGTGGCGCC 971
QY 260 oAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAs 280
Db 972 TAATTTACTGTTACCGCTGTGGTAAACATGGCTGTATTCTTGNATCGGGGAAACATGGA 1031
QY 280 nArgSerPheLeuGlnPheGluProAlaProArg-GlnSerGluProAspValThrArgL 300
Db 1032 CCAGAACTTCCTTCAATTCACCCCGCACCTCGGGCAAATTTGAGCGACACAACTCGCA 1091
QY 300 yThrProAspTyrPheLeu 306
Db 1092 AAACCCAGACTACTTTCTG 1111
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RESULT 15

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US-10-425-115-160546
; Sequence 160546, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TYPE: DNA
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160546
; LENGTH: 1759
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_77998C.1
US-10-425-115-160546
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Alignment Scores:

Pred. No.:	7,6e-187	Length:	1759
Score:	1456.00	Matches:	272
Percent Similarity:	75.45%	Mismatches:	23
Best Local Similarity:	69.57%	Indels:	11
Query Match:	87.19%	Gaps:	85
DB:	8		1
US-10-764-259-13 (1-306) x US-10-425-115-160546 (1-1759)			
QY 1	MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys		eu 20
Db 327	ATGCCATCGCAGCGGATCTCGACCGCCAGATCTCGCAGCTGCGGGATTG		TG 386
QY 21	SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa		rp 40
Db 387	CTGAGGCGGAGGTCAAAACCGCTATCGAGCAGGCCAAGGCGATCTCTCAI		3G 446
QY 41	AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln		is 60
Db 447	AACGTGACGCGGTGGTTCCTGCTGCTGCGGCGACATCCACGG		: : AC 506
QY 61	AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyr		et 80
Db 507	GACCTCATCGAGCTCTTTCGCATCGTGGCGACGCGCCGACACCAACT?		: : TG 566
QY 81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe		eu 100
Db 567	GGCAGCTACGTGACCGTGGCTACTACTCAGTGAGAGACTGTGCTTATTT		TA 626
QY 101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe		le 120
Db 627	AAAGTACGTTATAGACAGAGAATCACAAATTTGAGAGGAAATCATGAGAG		: : TA 686
QY 121	ThrGlnVal-----		-- 123
Db 687	ACTCAAGTGTATGGCTTCTATGATGAATGCTTGGGAAATATGGAATGTC		GG 746
QY 123	-----		-- 123
Db 747	AAGTACTTTACAGACTTGGTTGATTTATTTGTTGATTTTCAGATGGAAAAAT		CT 806
QY 123	-----		-- 123
Db 807	ACTGTAGATTTCAGATGTGGATAACTGACAGGATATAGAATTCGGAACCTG		3A 866
QY 123	-----		-- 123
Db 867	TCACTTGGTCTGGTTTCTAACTGTAGGACATTATAGTGCATGTTTATCA		CC 926
QY 124	-----TyrGlyPheTyrAspGluCysLeuArgI		As 136
Db 927	CTTGACAAACATTTCCCAAGGTATGGCTTCTATGATGAATGCTTTCGGA		AA 986
QY 136	nAlaAsnValTrpLysTyrPheThrAspLeuPheAspTyrLeuProLeuI		Il 156
Db 987	TGCAAAATGTGTGGAAGTACTTTTACAGACTTGTGTTGATTTTGGCTCTCA		AT 1046
QY 156	eGluHisGluIlePheCysLeuHisGlyLysSerProSerLeuAspI		Hi 176
Db 1047	AGAAAATCAGATCTCTCGCTACATGGTGGTCTCTCTCCATCACTGGATA		: : AA 1106
QY 176	sIleArgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetC		Le 196
Db 1107	TGTCGGTCCCTTGATCGCATACAGAGTCCCGCATGAAGACCTATGT		TT 1166
QY 196	uTrpSerAspProAspArgCysGlyTrpGlyIleSerProArgGlyA		Th 216
Db 1167	GTGGTCTGACCCGGATGACAGATGTGGATGGGAAATTCACCAAGGGGTG		AC 1226
QY 216	rPheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerI		Ar 236
Db 1227	ATTTGGCCAAAGATATTGCACAACAAAATTCACCAATACAAATGGGCTAAGTC		: : AG 1286

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Qy 236 gAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrVa 256
Db 1287 AGCTCATCAACTTGAATGGAAGGGTTCAATTGGTGCCAGGATAAGAACGTTGTGACAGT 1346

Qy 256 lPheSerAlaProAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAs 276
Db 1347 GTTCAGCGCGCTAACTATTGCTACCGATGCGGAAACATGGCTGCCATCCTCGAAATTGG 1406

Qy 276 pGluThrMetAsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAs 296
Db 1407 CGAGAACATGGATCAGAACTTCCTCCAATTCGACCCAGCTCCGCGGCAGATTGAGCCGGA 1466

Qy 296 pValThrArgLysThrProAspTyrPheIeu 306
Db 1467 CATGACGCGCAAGACCCAGACTACTTTTGT 1497

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Search completed: December 9, 2005, 13:12:22
Job time : 833 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:37:52 ; Search time 248 Seconds
(without alignments)
461.288 Million cell updates/sec

Title: US-10-764-259-13
Perfect score: 1670
Sequence: 1 MFSYADVDRQIEQLSECKL.....BPAPRQSPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+p2n.model -DEV=xlp
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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10764259 @CGN 1.1.184 @runat_05122005_094549_7109
-NCPUI=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New.*

- 1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	84.5	1541	6	US-10-909-125-814 Sequence 814, App
2	111.5	6.7	3342	6	US-10-750-185-59362 Sequence 59362, A
3	107.5	6.4	1364	6	US-10-750-185-37665 Sequence 37665, A
4	96.5	5.8	1147	6	US-10-750-185-37096 Sequence 37096, A
5	93	5.6	1861	6	US-10-750-185-62270 Sequence 62270, A
6	89	5.3	728	6	US-10-750-185-37667 Sequence 37667, A
7	87.5	5.2	828	6	US-10-467-657-2501 Sequence 2501, Ap
8	87.5	5.2	963	6	US-10-467-657-2503 Sequence 2503, Ap

c	9	87	5.2	491	6	US-10-750-185-3553	Sequ
	10	87	5.2	753	7	US-11-135-855-18	Sequ
	11	87	5.2	163162	7	US-11-121-086-66	Sequ
c	12	86	5.1	2348	6	US-10-750-185-33466	Sequ
	13	82.5	4.9	2401	6	US-10-955-054A-137	Sequ
	14	82.5	4.9	2740	6	US-10-955-054A-101	Sequ
	15	82.5	4.9	191797	7	US-11-121-086-13	Sequ
	16	82	4.9	157224	7	US-11-112-908-51	Sequ
	17	82	4.9	161726	7	US-11-112-908-48	Sequ
	18	82	4.9	161726	7	US-11-112-908-52	Sequ
	19	82	4.9	170189	7	US-11-112-908-50	Sequ
	20	81.5	4.9	1272	6	US-10-467-657-2677	Sequ
c	21	81.5	4.9	3242	6	US-10-750-185-35660	Sequ
	22	80	4.8	2107	6	US-10-750-185-44725	Sequ
	23	80	4.8	3065	6	US-10-793-626-3730	Sequ
c	24	78	4.7	153142	7	US-11-121-086-27	Sequ
	25	77	4.6	2530	6	US-10-821-234-276	Sequ
c	26	77	4.6	3242	6	US-10-793-626-3733	Sequ
	27	76.5	4.6	1878	6	US-10-467-657-6425	Sequ
	28	76.5	4.6	1878	6	US-10-467-657-7617	Sequ
	29	76.5	4.6	2091	7	US-11-029-003-9	Sequ
c	30	76.5	4.6	3730	6	US-10-485-517-116	Sequ
	31	76	4.6	792	6	US-10-467-657-6939	Sequ
	32	76	4.6	963	6	US-10-750-185-46644	Sequ
	33	75.5	4.5	2031	7	US-11-058-727-51	Sequ
	34	75.5	4.5	2031	7	US-11-058-727-83	Sequ
	35	75.5	4.5	2031	7	US-11-108-389-51	Sequ
	36	75.5	4.5	2031	7	US-11-108-389-83	Sequ
c	37	74.5	4.5	1157	6	US-10-750-185-34749	Sequ
	38	74.5	4.5	1380	6	US-10-793-626-1245	Sequ
	39	74.5	4.5	1380	6	US-10-793-626-2553	Sequ
	40	74.5	4.5	1534	6	US-10-750-185-38375	Sequ
c	41	74.5	4.5	2998	6	US-10-793-626-3506	Sequ
c	42	74.5	4.5	3527	6	US-10-793-626-3890	Sequ
	43	74	4.4	1557	6	US-10-793-626-505	Sequ
	44	74	4.4	1693	6	US-10-750-185-50007	Sequ
c	45	74	4.4	3202	6	US-10-793-626-3386	Sequ

ALIGNMENTS

RESULT 1

US-10-909-125-814
; Sequence 814, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eige
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For
; FILE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: IGIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 814

; LENGTH: 1541

; TYPE: DNA

; ORGANISM: H. sapiens

US-10-909-125-814

Alignment Scores:

Pred. No.: 1.5e-171 Length: 1541
Score: 1411.00 Matches: 248
Percent Similarity: 93.69% Conservative: 34
Best Local Similarity: 82.39% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-909-125-814 (1-1541)

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Qy      6 AspValAspArgGlnIleGluClnLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db      46 GAGCTGGACCACTGGGTGGAGCAGCTGAACGAGTGTAAAGCTGAACGAGAACCAAGTG 105
Qy     26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValClnProVal 45
Db     106 CGGACGCTGGCAGAGCAAGCAAAATTTTAAACAAGAATCAATGTCAGAGGTT 165
Qy     46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuGluLeu 65
Db     166 CGTTCCTCTGTTACTGTCTGGAGATGTCATGTCATCAATTTTCATGATCTTTATGGAATC 225
Qy     66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
Db     226 TTTAGAAATGGTGGAAATACCCGATACAACTACTTATTCATGGGTGACTATGTAGAC 285
Qy     86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105
Db     286 AGAGATATTATTCACTGGAGACTGTGACTCTTCTGTAGCATTAAGAGTGGTTATCCA 345
Qy    106 AspArgIleThrIleLeuArgGlyAsnHisGlnSerArgGlnIleThrGlnValTyrGly 125
Db    346 GAACGCATTACAAATATTGAGAGGAATCACGAAGCCGACAAATTTACCAAGTATATGGC 405
Qy    126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp 145
Db    406 TTTTATGATGAATGTCGGAAGATGGGAATGCCAATCGTTTGAATAATTTTACAGAT 465
Qy    146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
Db    466 CTCCTTTGATTATCTCCACTTACAGCTTTAGTAGATGGACAGATATTCTGCCTCCATGTT 525
Qy    166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu 185
Db    526 GGCCTCTCTCCATCCATAGACACACTGGATCATATAAGAGCCCTGGATCGTTTACAGAA 585
Qy    186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly 205
Db    586 GTTCCACATGAGGCCCAATGTTGATCTGTTATGGTCAGATCCAGATGATCGTGGTGA 645
Qy    206 TrpGlyIleSerProArgGlyValaglyTyrThrPheGlyGlnAspIleAlaGluGlnPhe 225
Db    646 TGGGGTATTTCACCACTGGTGTCTGCTGCTACACATTTGGACAGACATTTCTGAAACCTTT 705
Qy    226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
Db    706 AACCATGCAATGGTGTCTCAGCTGTTTCTCGTGGCCACCAGCTTTGTAATGGAGGGATAC 765
Qy    246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db    766 AATTGGTGTGATTCGGAATGGTGTGTACCATTTTCAGTGCACCAATTAATCTGTTATCGT 825
Qy    266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db    826 TGTGGGAACAGGCTGCTATCATGAAATTAGATGACACTTTTAAATAATTTCTCTTCTCAA 885
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Qy     286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
Db     886 TTTGACCGCGCGCTCGTGGTGGAGCCTCATGTTACACGCGCACCCC 945
Qy     306 Leu 306
Db     946 CTA 948

RESULT 2
US-10-750-185-59362
; Sequence 59362, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 59362
; LENGTH: 3342
; TYPE: DNA
; ORGANISM: Bovine 19866880635842
US-10-750-185-59362

Alignment Scores:
Pred. No.: 0.00451 Length: 3342
Score: 111.50 Matches: 64
Percent Similarity: 44.29% Conservative: 29
Best Local Similarity: 30.48% Mismatches: 80
Query Match: 6.68% Indels: 39
DB: 6 Gaps: 8

US-10-764-259-13 (1-306) x US-10-750-185-59362 (1-3342)

Qy     56 HisGlyGlnPheHisAspLeuIleGluLeuPheArgIle-GlyGlyLysA 75
Db    1453 CACGTCATTTCTAGATGCTACCACGTCCTTTAGAACTGAGGGGAAAGA 1512
Qy     75 rAsnTyrLeuPheMetGlyAsp-----TyrV; 87
Db    1513 GAATTTATGTACATGTGGGTAATATGAGGGCTTCTCTGTAGCTCAGTGG 1572
Qy     87 yTyr-Tyr-SerValGluThrVal-----SerLeuL 100
Db    1573 GCCTGTAACACAGGAACCCCTGGTAAGATGAAGACAGCATAGACTGTGGC 1632
Qy    100 uLysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluS 120
Db    1633 TAGAGGGTCAGAAATTAGAGACTCTAACACAGCATTGAAGAGCAATGAAG 1691
Qy    120 eThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnA 140
Db    1692 TAACCAAGTGTGACATTTTATGATGGCTGT---TGAGAGTAAGACATG 1748
Qy    140 pLysTyr-PheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG 160
Db    1749 GGAAGTATTACAGACATGATGTGTTCTTCTCTCTGGGCACTGGTC- 1797
Qy    160 ePheCysLeuHisGly-GlyLeuSerProSerLeuAspThr-----Leu 185
Db    1798 ----TGT-----GGGTAACCTCCTCTGTTTCACAGACACACCTCCCTG 1847
Qy    178 rgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetCysAsp 197
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Db 1848 CAGTCTCGATCTTTCTGAGGC-----TCATCTCTGATCTTAC 1886
Qy 198 SerAspPro---ApsAsArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyThr 216
Db 1887 TCATCTCCTGAGATGGTCAGCTAAGCTGGGGTTTTCTTA-CAAGGCACCTGCGTGAC 1945
Qy 217 PheGlyGlnAspIleAlaGluGlnPheAenHisThrAenGlyLeuSer-LeuValAlaAr 236
Db 1946 TTTGAACAAGACATTTCCGAGACTCTAGCCATCCCGAGCTCTCTGGCTTCTACACA 2005
Qy 236 GALAHISGlnLeuValMetGlu 243
Db 2006 CGTTCACCCACTTGCCCTGGAG 2027

RESULT 3
; Sequence 37665, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37665
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Bovine 19866880394924
US-10-750-185-37665

Alignment Scores:
Pred. No.: 0.00661 Length: 1964
Score: 107.50 Matches: 25
Percent Similarity: 43.59% Conservative: 9
Best Local Similarity: 32.05% Mismatches: 13
Query Match: 6.44% Indels: 31
DB: Gaps: 2

US-10-764-259-13 (1-306) x US-10-750-185-37665 (1-1964)
Qy 101 LysValArgTyrArgAspArgIleThrLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 1018 AAAATAAAGTATTCAAGCGCGTA----- 1041
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db 1042 -----TATGATGCTGCATG----- 1056
Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db 1057 -----GATGCTTTGACTGCTGCGCTGCTGCTGATGATGATGATGATGATGAT 1104
Qy 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArg 178
Db 1105 CCTGTGTGTACGGCGGTTTGTCTCCAGAGATAAACACTTTTAGATGATATCAGA 1158

RESULT 4
US-10-185-37096/c
; Sequence 37096, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
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; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37096
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Bovine 19866880767627
US-10-750-185-37096

Alignment Scores:
Pred. No.: 0.0771 Length: 1147
Score: 96.50 Matches: 17
Percent Similarity: 62.50% Conservative: 8
Best Local Similarity: 42.50% Mismatches: 8
Query Match: 5.78% Indels: 7
DB: Gaps: 1

US-10-764-259-13 (1-306) x US-10-750-185-37096 (1-1147)
Qy 44 ProValLysCysPro-----ValThrValCysGln 56
Db 1022 CCTCTCGCGGCGCTCTTTTCTCCAGACAGAGAAGATTACAGTGTGCGG 963
Qy 57 GlyGlnPheHisAspLeuIleGluLeuPheArgIleGlyGlyLysAlaPr 76
Db 962 GCCCAGTTCTATGACCTCTGACATATTTGAGCTCAACGGTTTACCCTC 903

RESULT 5
US-10-750-185-62270
; Sequence 62270, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62270
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Bovine 19866880123096
US-10-750-185-62270

Alignment Scores:
Pred. No.: 0.456 Length: 1861
Score: 93.00 Matches: 16
Percent Similarity: 86.36% Conservative: 3
Best Local Similarity: 72.73% Mismatches: 3
Query Match: 5.57% Indels: 0
DB: Gaps: 0

US-10-764-259-13 (1-306) x US-10-750-185-62270 (1-1861)
```

QY 59 PheHisAspLeuLeuGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeu 78
 Db 1636 TTTTATGACCTTTGTGAACCTGTCAGAACTGGAGGTCAGGTTCTCTGACACAAACTACATA 1695

QY 79 PheMet 80
 Db 1696 TTTATG 1701

RESULT 6

US-10-750-185-37667
 ; Sequence 37667, Application US/10750185
 ; Publication No. US20050260603A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MW1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIORITY FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37667
 ; LENGTH: 728

; TYPE: DNA

; ORGANISM: Bovine 19866880838231

US-10-750-185-37667

Alignment Scores:
 Pred. No.: 0.36 Length: 728
 Score: 89.00 Matches: 15
 Percent Similarity: 80.95% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 4
 Query Match: 5.33% Indels: 0
 DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-750-185-37667 (1-728)

QY 180 LeuAspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTyrSerAsp 199
 Db 650 TTAGACCGATTCAAGAACCACTGCTTATGGACCTATGTGTGATATCTGTGGTCAGAC 709

QY 200 Pro 200
 Db 710 CCG 712

RESULT 7

US-10-467-657-2501

; Sequence 2501, Application US/10467657
 ; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWing99, version 1.04
 ; SEQ ID NO 2501
 ; LENGTH: 828

; TYPE: DNA
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2501

Alignment Scores:

Pred. No.: 0.684 Length: 828
 Score: 87.50 Matches: 52
 Percent Similarity: 35.58% Conservative: 22
 Best Local Similarity: 25.00% Mismatches: 69
 Query Match: 5.24% Indels: 65
 DB: 6 Gaps: 10

US-10-764-259-13 (1-306) x US-10-467-657-2501 (1-828)

QY 53 GlyAspIleHisGlyGlnPheHisAspLeuLeuGluLeuPhe---ArgIl.
 Db 19 GGCACATCCAAGGCTGTTTCGACGAACTGACCGCGCTCGGCAAAAT.
 QY 71 LysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgGl.
 Db 79 CACGGCACGGACACCTCTGGCTG---ACGGCGCACATCGTCAACCGCG.
 QY 91 ValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspAr.
 Db 136 CTCGAACGCTGCAATTCTGTC-----ATCGGCGACGAAACAG.
 QY 111 LeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTy.
 Db 184 GTCCTCGGCAACACGAC-----
 QY 131 LeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPh.
 Db 202 -----
 QY 151 ProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLe.
 Db 205 TACCTGCTCGCC-----GTCGGCTCGCGGAGGCGCGCT.
 QY 171 LeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluValPr.
 Db 250 ---GACACA-----ATCGAACCCATATACTCAAAACACCC.
 QY 191 ProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGlyTrpGl.
 Db 289 AAAATGCTCGACTCGCTCGCGCGCAACCG-----CT.
 QY 211 ArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsnHi.
 Db 331 GAGGCGCGCGCTGATCATACACCGCGCATCTCGCGCAATGGCGC--
 QY 231 LeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTr.
 Db 379 -----ATAGCCAAAGCCGAATCGCTCGCGGAGAGCGGAAAGCGGA.
 QY 251 LysAsnValValThrValPheSer 258
 Db 430 AAAAAATACGTCAAATCTTCTCC 453

RESULT 8

US-10-467-657-2503/c

; Sequence 2503, Application US/10467657
 ; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8

```

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2503
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2503

Alignment Scores:
Pred. No.: 0.861 Length: 963
Score: 87.50 Matches: 52
Percent Similarity: 35.58% Conservative: 22
Best Local Similarity: 25.00% Mismatches: 69
Query Match: 5.24% Indels: 65
DB: 6 Gaps: 10

US-10-764-259-13 (1-306) x US-10-467-657-2503 (1-963)
Qy 53 GlyAspIleHisGlyGlnPheHisAspLeuIleGluLeuPhe---ArgIleGly---Gly 70
Db 774 GCGACATCCAAAGCTGTTTCAGCAACTGACCGCGCTGCTCGGCAAAATCGGCTTCAC 715
Qy 71 LysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgGlyTyrTyrSer 90
Db 714 CACGGCAGCGACACCCCTCTGGCTG---ACGGCGACATCGTCAACCGCGCGCGCAAAATCC 658
Qy 91 ValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspArgIleThrIle 110
Db 657 CTCGAAGCGCTGCAATTCGCTG-----ATCCGGCGAGAAACACAGCGTGCAAATC 610
Qy 111 LeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCys 130
Db 609 GTCCTCGCAACACGAC-----592
Qy 131 LeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPheAspTyrLeu 150
Db 591 -----CTG 589
Qy 151 ProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLeuSerProSer 170
Db 588 TACCTGCTCGCC-----GTCCGCTCGCGCGAAGCGCGCTCAAAAGCGACG 544
Qy 171 LeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluValProHisGluGly 190
Db 543 ---GACACA-----ATCGAACCCATACTCAACACCCCGCGCGCGA 505
Qy 191 ProMetCysAspLeuLeuTrpSerAspProAspArgCysGlyTrpGlyIleSerPro 210
Db 504 AAAATGCTCGACTGGCTCGCGCGCAACCG-----CTTTTGATACGC 463
Qy 211 ArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGly 230
Db 462 GAGGCGCGCGCGGTGATGATACACCGCGCATCTCGCGCAATGGCG-----415
Qy 231 LeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAsp 250
Db 414 -----ATAGCAAAAGCGAATCGCTCGCGGAGAGCGGAGCGAAGCGAATCGCGCGC 364
Qy 251 LysAsnValValThrValPheSer 258
Db 363 AAAAAATACGTCAAAATCTTCTCC 340

RESULT 9
US-10-750-185-3553/c
; Sequence 3553, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3553
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Bovine MMBT13351
US-10-750-185-3553

Alignment Scores:
Pred. No.: 0.359 Length: 491
Score: 87.00 Matches: 19
Percent Similarity: 54.55% Conservative: 11
Best Local Similarity: 34.55% Mismatches: 23
Query Match: 5.21% Indels: 2
DB: 6 Gaps: 1

US-10-764-259-13 (1-306) x US-10-750-185-3553 (1-491)
Qy 94 ValSerLeuLeuValAlaLeuLysValArgTyrArgAspArgIleThrIle 113
Db 490 GTCTTATATTATGGTCTCGAAGATTCGTATCCAGTACATTATTTCT 431
Qy 114 AsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCys 133
Db 430 AACCATGAATGCAGACACCTTACTGAATATTTTACCTTTTAAGCAGGAATG 377
Qy 134 TyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPheAsp 148
Db 376 TACTGCATGAGAACTATTTTCACTTCTCCTCAGGGTTCTTTTAGAG 332

RESULT 10
US-11-135-855-18
; Sequence 18, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GF50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-18

Alignment Scores:
Pred. No.: 0.687 Length: 753
Score: 87.00 Matches: 49
Percent Similarity: 35.14% Conservative: 29
Best Local Similarity: 22.07% Mismatches: 80
Query Match: 5.21% Indels: 64
DB: 7 Gaps: 11

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US-10-764-259-13 (1-306) x US-11-135-855-18 (1-753)
Qy 111 LeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCys 130
Db 82 ATGAATGCCAACACCAACAGAGAGTGCAGCCAGCCAGAGCAAGCTCTATGAGGAGTGC 141
Qy 131 LeuArgLysTyrGlyAsnAla-----AsnValTrpLysTyrPheThrAsp 145
Db 142 ATCCCTCGAAGGACAAATGCGCTGTCACCTCACGACAAGCTGGAA----- 189
Qy 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
Db 190 -----GCCATCTGGATATCCCACTCTACAACTTCAGCCTGTT-----CACGTG 237
Qy 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGln 185
Db 238 GGACTGCTGATGCTGGCTGTGCGAAGCACATTATCCAGGCTATCTGCTTCTATGAGTGC 297
Qy 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly 205
Db 298 TCCCCAAACCTGGGGCCC-----TGGATCCAGCCAGTGGGAAGCCTGGGG 342
Qy 206 TrpGlyIleSerProArgGlyAlaGly-----TyrThrPheGlyGlnAsp 220
Db 343 TGGGAGGTGGCCCCGAGTGGGCGAGGAGCGAGTGTGAATGTGCCCTGTGCCAGGAG 402
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaAlaHisGlnLeu 240
Db 403 GACTGTGAGGAGTGTGGGAAGACTGTGCGCATGTCTTACACATGCATAATCCAACTGG-- 459
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 460 ---CGTGTGCTGGGACTGTGAGTGGAGGAGAAC----- 492
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIle----- 275
Db 493 -----CGCTGCCCAAGGGGCCCGCCGCTTCTCCCTTCTCCCTTACTTCCCC 540
Qy 276 -----AspGluThrMetAsnArgSerPhe----- 283
Db 541 ACCCGAGCTGACCTGTGTGAGAGAGACTGGAGCAATTCTTCAAAGCCAGCCCTGAGCGA 600
Qy 284 -----LeuGln-----PheGluProAlaProArgGlnSerGluPro 295
Db 601 CGGAACAGTGGCGGTGTCTCCAGAAAGTGTGTGAGCCTGCT-----CAGGGCAACCCC 654
Qy 296 AspVal 297
Db 655 AATGTG 660

RESULT 11
US-11-121-086-66
; Sequence 66, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIORITY FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 163162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-66
Alignment Scores: 2.45e+03 Length: 163162
Pred. No.: 163162
```

```
Score: 87.00 Matches: 57
Percent Similarity: 35.63% Conservative: 31
Best Local Similarity: 23.08% Mismatches: 74
Query Match: 5.21% Indels: 87
DB: 7 Gaps: 13

US-10-764-259-13 (1-306) x US-11-121-086-66 (1-163162)
Qy 24 GluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 43
Db 151928 GAAATAATGATATGACAGAGCAGTGCAGTACTAGTGTGACCATG-----TG 151981
Qy 44 ProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 63
Db 151982 GCTTACAAAGTGTATGATT---GTGTGAGCGCACAAACACGCATGGGAAG 152038
Qy 64 GluLeuPheArgIleGlyGlyLysAlaProAsp-----ThrAsp 79
Db 152039 TCTCTT-----AGAGGAAAAATCCAGAACTCCAACGGCCACGTC 152085
Qy 80 MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeu 99
Db 152090 TTGACCAGCTCTGTG-----GCTTTGAGCACATGACTTCT 152134
Qy 100 LeuLysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGln 119
Db 152135 ATGTGCTTACTCTCAAAATGGGAGGAAACTGTCTCAGAGGTAATCATGA 152185
Qy 120 IleThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsp 139
Db 152186 -----GACGAG----- 152200
Qy 140 TrpLysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIle 159
Db 152201 TGG----- 152215
Qy 160 IlePheCys-----LeuHisGlyGlyLeu-----SerProSe 173
Db 152216 GTCATCTGTCAAAATGTAGTCCCTGGGAAGGTCAATAAGCAATCTCCATC 152275
Qy 174 LeuAspHisIleArgAlaLeuAspArgIleGlnGluValProHisGluGln 193
Db 152276 CTCCCCCACTTGCAC-----CCCCAC----- 152296
Qy 194 AspLeuLeuTrpSerAspProAspAspArgCysGlyTrpGlyIleSerPro 213
Db 152297 AACATGCTCAGGCCCCAGCCCAAGTGCCAAAGTGGGGTGGTGT--CC 152354
Qy 214 GlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGln 233
Db 152355 GGCTAC----- 152360
Qy 234 ValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAsp 253
Db 152361 ATGCCAGAGGTGCC-AGCTCAGGAGGACTGGTAGGATGGTGAGAGTG 152419
Qy 254 ValThrValPheSerAlaPro 260
Db 152420 GTGCCATACCTGTCTACTCCA 152440

RESULT 12
US-10-750-185-53466/c
; Sequence 53466, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-137

Alignment Scores:
Pred. No.: 15 3      Length: 2401
Score: 82.50      Matches: 66
Percent Similarity: 37.12%      Conservative: 68
Best Local Similarity: 18.84%      Mismatches: 156
Query Match: 4.94%      Indels: 72
DB: 6      Gaps: 13

US-10-764-259-13 (1-306) x US-10-955-054A-137 (1-2401)

Qy 4 TyzAlaAspValAspArgGlnIleGluInLeuSerGluCysLeysProLe
Db 1306 TATGCCATGGCTCCCGGAGCGTCTTCTCTCTGAA-GAATCAACCCGTCT
Qy 24 GluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGlu-
Db 1365 GGGCCTGGAAAGTCTATGTGACATTTCTCGAGATCTACAATGGGAAGCTGT
Qy 43 nProValLysCysProValThrValCysGlyAsp-
Db 1425 CAACAAGAGCCCAAGCTGCGCGTGTGGAGAGCGGCAAGCAACACAGGTGTC
Qy 56 sGlyGlnPheHis-----AspLeuIleGluLeuPheA
Db 1485 GCTGCAGAGCACTGGTTAACTCTGTGATGATGTCATCAAGATGCTCTC
Qy 70 yLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArg-
Db 1545 CGCCTGCAGAACCTCTGGCGAGACATTTGCCAACTCCAATTCCTCCCGCT
Qy 90 rValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspA
Db 1605 CTTCCAA-----ATTATCTTCGAGCTAAAGGGAGAAATGCATGGCA
Qy 110 e-----LeuArgGlyAsnHis-----
Db 1656 GTTAGTCTGGCAGGGAATGAGCGAGCGGCAGACACTTCCAGTGCTGACGACC
Qy 116 ----GluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCysI
Db 1716 CATGGAGGCGCGAGAAATCAACAAGAGTCTCTAGCCCTGAAGGAGTGCA
Qy 134 rGlyAsnAlaAsnValTrpLysTyrPheThrAsp-----LeuPheAspI
Db 1776 GGGACAGACAAGAGCTCACACCCCGTTCCGTGAGAGCAAGCTGACACAGG
Qy 152 uThrAlaLeuIleGluHisGluIlePheCysLeuHi sGlyGlyLeuSerF
Db 1836 CTCTCTCATTTGGGAGAACTCTAGGACTTGATGATTCCTCCACGATCTCAC
Qy 172 p-----ThrLeuAspHisIleArgAlaLeuAspArgIleGlnC
Db 1896 CTCCTGTGATATACTTTAAACACCCCTGAGATATGCACACAGGGTCAAGG
Qy 187 oHisGluGlyProMetCysAspLeuLeu-----TrpSerAspProA
Db 1956 CCACAGTGGGCCCAAGTGCAGAGCAGTTCGATTCAAATGGAAACACAGAAGAGA
Qy 204 sGlyTrpGlyLysSerProArgGlyAlaGlyTyrThrPheGlyGlnAspI
Db 2016 CTCTAACGGGGCGCTGATTCGAGGCAATTTATCCAAGGAAGAGGGAAC
Qy 224 nPheAsnHisThrAsnGlyLeuSerLeuValAlaArg-----
Db 2076 GATGTCAGCTTTAAACGAAGCCATGATCTCAGATCAGGAGCTGGAGGAGA
Qy 237 ----AlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysA
Db 2136 AGAGCTCAAGAGATCATACAGCAAGACCCAGATCGGCTCTCAG-----

```

RECORD IS
UUS-10-955-054A-137

Sequence 137. Application IIS/10955054A

: Publication No. US20050266420A1

GENERAL INFORMATION:

APPLICANT: PUSZTAI, LAJOS

APPLICANT: SYMMANS, W. FRASER

APPLICANT: HESS, KENNETH

; APPLICANT: AYERS, MARK

APPLICANT: STEC, JAMES

; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY

; FILE REFERENCE: UTXC:880U:

; CURRENT APPLICATION NUMBER: US/10/955,054A

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 195

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; SOFTWARE: PatentIn Ver. 2.1
;

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; SEQ ID NO 137

; LENGTH: 2401

```

QY 255 rValpHeSerAlaProAsnTyr----- 262
Db 2187 GATGACGAGCGAGCGAGTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCT 2246
QY 263 -CysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe 282
Db 2247 GCGCCAGCAAGCCAGCATTTCTGAGCCTCGGAGATGTCATCAAGGCTTTACGCTGGC 2306
QY 282 rPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 302
Db 2307 CATGCAGCTGGAAGAGCAGCGCTAGCAGACAAATAAGC-----AGCAAGAAACGGCC 2357
QY 302 p 302
Db 2358 C 2358

RESULT 14
US-10-955-054A-101
; Sequence 101, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 2740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-101

Alignment Scores:
Pred. No.: 18.7 Length: 2740
Score: 82.50 Matches: 68
Percent Similarity: 37.12% Conservative: 66
Best Local Similarity: 18.84% Mismatches: 156
Query Match: 4.94% Indels: 72
DB: 6 Gaps: 13

US-10-764-259-13 (1-306) x US-10-955-054A-101 (1-2740)

QY 4 TyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeu 23
Db 1174 TATGCGATGGCTCCCGGGAGCGTCTTCCTCCTGAA-GAATCAACCCCTGCTACCGGAAGTT 1232
QY 24 GluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGlu-TyrAsnValGl 43
Db 1233 GGGCTGGAAGTCTATGTGACATTTTCGAGATCTACATGGGAAGCTGTTGACCTGCT 1292
QY 43 nProValLysCysProValThrValCysGlyAsp-----IleHi 56
Db 1293 CAACAAGAAGCGCAAGCTCGCGTCTGGAGGCGGCAAGCAAGGTGCAAGTGGTGGG 1352
QY 56 sGlyGlnPheHis-----AspLeuIleGluLeuPheArgIleGlyGl 70
Db 1353 GCTCGAGGAGCATCTGGTTAACTCTGATGATGTCATCAAGATGCTCGACATGGCGAG 1412
QY 70 yLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgGlyTyrTyrSe 90
Db 1413 GCGCTGGAAGCTTCGGCGAGACATTTGCCAACTCCCAATTCCTCCCGCTCCACGCGTG 1472
QY 90 rValGluThrValSerLeuLeuAlaLeuLysValArgTyrArgAspArgIleThrIl 110
Db 1473 CTTCCAA-----ATTATTCTTCGAGCTAAAGGGAGATGATGGAAGTTCTCTTT 1523

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QY 110 e-----LeuArgGlyAsnHis----- 115
Db 1524 GGTAGATCTGCGAGGAATGAGCGAGCGGAGACACATCTTCCAGTGTGACAC 1583
QY 116 ---GluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCysL 134
Db 1584 CATGAGGCGGCGCAGAAATCAACAGAGTCTCTTAGCCCTGGAAGGAGTGCA 1643
QY 134 rGlyAsnAlaAsnValTrpLysTyrPheThrAsp-----LeuPheAspT 152
Db 1644 GGGACAGAACAAAGCTCACACCCGTTCCGTGAGCAAGCAAGCTGACACAGG 1703
QY 152 uThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLeuSerP 172
Db 1704 CTCCTTCATTTGGGGAACCTCTAGGACTTGATGATTCGCCACGATCTCAC 1763
QY 172 p-----ThrLeuAspHisIleArgAlaLeuAspArgIleGlnG 187
Db 1764 CTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGGTCAAGG 1823
QY 187 oHisGluGlyProMetCysAspLeuLeu-----TrpSerAspProAl 204
Db 1824 CCACAGTGGGCGCCAGTGGAGAGCAGTTTCATTCAAAATGGAACACAGAGAGA 1883
QY 204 sGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspi 224
Db 1884 CTCTAAGCGGGCGCTGATTCAGGCAATTTATCCAAAGAGAGGAGGAAC 1943
QY 224 nPheAsnHisThrAsnGlyLeuSerLeuValAlaIleAarg----- 236
Db 1944 GATGTCAGCTTTTAAACGAGCCATGACTCAGATCAGGAGCTGGAGGAGA 2003
QY 237 ---AlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysAl 255
Db 2004 AGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGGCTTGAG----- 2054
QY 255 rValPheSerAlaProAsnTyr----- 262
Db 2055 GATGACCGAGCAGCCAGACTATGACTGGAGACCTTTGTGAACAAAGCGG 2114
QY 263 -CysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrM 282
Db 2115 GGCCCGACCAAGCAGCATTTCTCAGCCCTCGAGATGTCATCAAGGCGCT 2174
QY 282 rPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrA 302
Db 2175 CATGCAGCTGGAAGAGCAGGCTAGCAGACAAATAAGC-----AGCA 2225
QY 302 p 302
Db 2226 C 2226

RESULT 15
US-11-121-086-13
; Sequence 13, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANAL
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 191797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-13

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Alignment Scores:

Pred. No.:	1.19e+04	Length:	191797
Score:	82.50	Matches:	40
Percent Similarity:	35.80%	Conservative:	18
Best Local Similarity:	24.69%	Mismatches:	59
Query Match:	4.94%	Indels:	46
DB:	7	Gaps:	7

US-10-764-259-13 (1-306) x US-11-121-086-13 (1-191797)

Qy	126	PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPhe---	Thr 144
Db	154760	TTTCGGGTGACACCTTTAGGAGGTACGGGGATTAAACAAATATTTTACTTCCAGTT	154819
Qy	145	AspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHis	164
Db	154820	CCCCACCTCTGCTATCACCTCTCACAACTTCATCCAGCATCAGCTTCTTTCG----	154873
Qy	165	GlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAla-LeuAspArgIleGl	184
Db	154874	-----CCTAAATTTAATCGTCATCTTATAAACTTGCTATTGCAAGAATAT	154921
Qy	184	nGluValPro-----HisGluGlyPro-----	191
Db	154922	AAATATTCCTTTAACTGTGTAATGCTCTTTCAAACCATGGTCCCAAAATCCTCTACTA	154981
Qy	192	-----MetCysAspLeuLeuTrpSerAspProAspAsp-----	ArgCy 204
Db	154982	AAATTAAGCCTTCTTCCCAAGCATCTGGTGCCATAGCCATAGTCTTTTGAATG	155041
Qy	204	sGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGl	224
Db	155042	GGCTTGGGGAGATAATATATTACCAGGGCTTTACCATGGCTTTATCCATAGAGACTA	155101
Qy	224	nPheAsnHisThrAenGlyLeuSerLeuValAlaAlaArgAlaHisGlnLeuValMetGluGl	244
Db	155102	GTTTAACAGAAAGCTT-GGC-----	155130
Qy	244	yTyrAsnTrp-----CysGlnAspLysAsnValValThrValph	257
Db	155131	AGTGAATGGCAGCCCAACAGGAGCAAGCTGTGTGAGGACAAATGTACACTCTCCATTTT	155190
Qy	257	eSer 258	
Db	155191	CTCT 155194	

Search completed: December 9, 2005, 13:18:29
Job time : 363 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 09:50:51 ; Search time 163 Seconds
(without alignments)
1324.489 Million cell updates/sec

Title: US-10-764-259-13

Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1548	92.7	306	Q6VU05_LYCERS	Q6VU05 lycopersico
2	1538	92.1	306	Q9MB06_VICFA	Q9MB06 vicia faba
3	1534	91.9	306	Q6VU06_LYCERS	Q6VU06 lycopersico
4	1526	91.4	306	Q9FSV3_FAGSY	Q9FSV3 fagus sylv
5	1522	91.1	306	P2A1_ARATH	Q07098 arabidopsis
6	1519	91.0	306	Q9MB05_VICFA	Q9MB05 vicia faba
7	1514	90.7	306	Q8LAW8_ARATH	Q8LAW8 arabidopsis
8	1512	90.5	306	Q527K2_ORYSA	Q527K2 oryza sativ
9	1509	90.4	306	P2A3_HEYBR	Q9Z8E4 hevea brasl
10	1508.5	90.3	307	P2A3_ORYSA	Q9Z8E7 oryza sativ
11	1508.5	90.3	307	Q6Z6L9_ORYSA	Q6Z6L9 oryza sativ
12	1508	90.3	306	P2A2_ARATH	Q07099 arabidopsis
13	1506	90.2	306	P2A1_ORYSA	Q9Z8E3 oryza sativ
14	1501.5	89.9	305	P2A5_HELAN	P48579 helianthus
15	1495	89.5	307	P2A5_ARATH	Q04951 arabidopsis
16	1481	88.7	306	Q42981_ORYSA	Q42981 oryza sativ
17	1445	86.5	302	Q04859_TOBAC	Q04859 nicotiana t
18	1427	85.4	309	P2AA_BOVIN	P67774 bos taurus
19	1427	85.4	309	P2AA_HUMAN	P67775 homo sapien
20	1427	85.4	309	P2AA_MOUSE	P63330 mus musculu
21	1427	85.4	309	P2AA_PIG	P67776 sus scrofa
22	1427	85.4	309	P2AA_RABIT	P67777 oryctolagus
23	1427	85.4	309	P2AA_RAT	P63331 rattus norv
24	1427	85.4	309	Q58D70_BOVIN	Q58D70 bos taurus
25	1427	85.4	309	Q4RSN5_MACFA	Q4RSN5 m brain cdn
26	1427	85.4	309	Q5SNT5_MOUSE	Q5SNT5 mus musculu
27	1426	85.4	309	Q8WN16_CANFA	Q8WN16 canis faml1
28	1425	85.3	294	Q6Z6L8_ORYSA	Q6Z6L8 oryza sativ
29	1424	85.3	309	Q6P365_XENTR	Q6P365 xenopus tro
30	1424	85.3	309	Q5ZM47_CHICK	Q5ZM47 gallus gall
31	1421	85.1	309	Q8AVH9_XENTR	Q8AVH9 xenopus lae

32	1419	85.0	309	Q619T8_HUMAN	Q619T8
33	1419	85.0	309	Q7ZVE7_BRARE	Q7ZVE7
34	1414.5	84.7	309	P2AA_CHICK	P4846
35	1413	84.6	306	Q5KGH3_CRYNE	Q5KGH3
36	1413	84.6	309	Q7PD38_ANOGA	Q7PD38
37	1412	84.6	309	P2A3_PROME	P2365
38	1411	84.5	309	P2AB_HUMAN	P6271
39	1411	84.5	309	P2AB_MOUSE	P6271
40	1411	84.5	309	P2AB_RABIT	P6271
41	1411	84.5	309	P2AB_RAT	P6271
42	1411	84.5	309	Q8WZ56_HUMAN	Q8WZ56
43	1411	84.5	309	Q6P3K5_HUMAN	Q6P3K5
44	1411	84.5	309	Q803G3_BRARE	Q803G3
45	1410	84.4	309	Q6GLE6_XENTR	Q6GLE6

ALIGNMENTS

RESULT 1
Q6VU05_LYCERS
ID Q6VU05_LYCERS PRELIMINARY; PRT; 306 AA.

AC Q6VU05;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Protein phosphatase 2A catalytic subunit.
GN Name=PP2Ac2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopers
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15125764; DOI=10.1111/j.1365-3113.2004.02073.x;
RA He X., Anderson J.C., del Pozo O., Gu Y.-Q., Tang X., Marti
RT "Silencing of subfamily I of protein phosphatase 2A catalyt
RT results in activation of plant defense responses and local i
death.";
RL Plant J. 38:563-577(2004).
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC phosphate.
CC -I- SIMILARITY: Belongs to the PPP phosphatase family.
CC EMBL; AY325818; AAQ67226.1; -; mRNA.
DR HSSP; Q08209; 1AUI.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STEPHITASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN 1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 35009 MW; C0719F26F8FCA0E5 CRC64;

Query Match 92.7%; Score 1548; DB 2; Length 306
Best Local Similarity 91.2%; Pred. No. 4.2e-129;
Matches 279; Conservative 15; Mismatches 12; Indels

QY	1	MFSYADVDRQIEQLSECKPLSELEVKNCDOARTTLVEBMNVQPKCPVT	1	Q6VU05_LYCERS	Q6VU05 lycopersico
DB	1	MFSYADVDRQIEQLSECKPLSEADVKTCDQAFALIVEBMNVQPKCPVT	1	Q6VU06_LYCERS	Q6VU06 lycopersico
QY	61	DLIEIFRIGKAPDNNYIFPMGDYVDRGYYSVETVSLVALKVRVDRRTI	61	P2AA_MOUSE	P63330 mus musculu
DB	61	DLIEIFRIGKAPDNNYIFPMGDYVDRGYYSVETVSLVALKVRVDRRTI	61	P2AA_MOUSE	P63330 mus musculu
QY	121	TQVGFYDECKRKGNANVMKXFTDLPDYLPALTALIEHIFCLHGLSPS	121	Q6Z6L8_ORYSA	Q6Z6L8 oryza sativ
DB	121	TQVGFYDECKRKGNANVMKXFTDLPDYLPALTALIEHIFCLHGLSPS	121	Q6Z6L8_ORYSA	Q6Z6L8 oryza sativ

its

8 0;
FH 60
FY 60
OI 120
OI 120
AL 180
AL 180
AL 180

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QY 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIAEQFNHTGLSVARAHOL 240
DB 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIASQFNHTGLTISARAHOL 240
QY 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAPROSEPVTTRK 300
DB 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAPROSEPVTTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 2
Q9MB06_VICFA PRELIMINARY; PRT; 306 AA.
ID Q9MB06_VICFA PRELIMINARY; PRT; 306 AA.
AC Q9MB06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type 2A protein phosphatase-1.
GN Name=vfpp2ac-1;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ueno H., Kinoshita T., Asanuma M., Shimazaki K.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AB039916; BA092697.1; -; mRNA.
DR HSSP; P36873; 1176.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 34954 MW; 30C13CCDAB495DE7 CRC64;

Query Match 92.1%; Score 1538; DB 2; Length 306;
Best Local Similarity 90.8%; Pred. No. 3.3e-128;
Matches 278; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVTVCSDIHGQTH 60
DB 1 MFSHADVDRIQLMECKPLSEAEVKTLCQARAILVEEMNVQPVKCPVTVCSDIHGQTH 60
QY 121 TVYGGFYDECLRKRYGNANWKYFTDLFDYLPALTALIEHIEFCLHGLSPSLDTLDIRAL 180
DB 121 TVYGGFYDECLRKRYGNANWKYFTDLFDYLPALTALIESQIFCLHGLSPSLDTLDIRAL 180
QY 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIAEQFNHTGLSVARAHOL 240
DB 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIAEQFNHTGLTISARAHOL 240
QY 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAPROSEPVTTRK 300
DB 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAPROSEPVTTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
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DB 301 TPDYFL 306

RESULT 3
Q6VU06_LYCSES PRELIMINARY; PRT; 306 AA.
ID Q6VU06_LYCSES PRELIMINARY; PRT; 306 AA.
AC Q6VU06;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein phosphatase 2A catalytic subunit.
GN Name=PP2AC1;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopers
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15125764; DOI=10.1111/j.1365-3113X.2004.02073.x;
RX He X., Anderson J.C., del Pozo O., Gu Y.-O., Tang X., Marti;
RT "Silencing of subfamily I of protein phosphatase 2A catalyt
RT results in activation of plant defense responses and local
RT death."
RL Plant J. 38:563-577(2004).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei;
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AY325817; AA067225.1; -; mRNA.
DR HSSP; Q08209; 1AUI.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 35068 MW; 846BD5A03F63B107 CRC64;

Query Match 91.9%; Score 1534; DB 2; Length 306
Best Local Similarity 91.2%; Pred. No. 7.4e-128;
Matches 279; Conservative 12; Mismatches 15; Indels 3;

QY 1 MFSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVT 3H 60
DB 1 MFSHADVDRIQLMECKPLSEAEVKTLCQARAILVEEMNVQPVKCPVT 1Y 60
QY 61 DIIEIFRIGKAPDNTNYLFMGDYVDRGYYSVETVSLVLAKVRYRDRITL 2I 120
DB 61 DIIEIFRIGKAPDNTNYLFMGDYVDRGYYSVETVSLVLAKVRYRDRITL 2I 120
QY 121 TVYGGFYDECLRKRYGNANWKYFTDLFDYLPALTALIEHIEFCLHGLSPS 2L 180
DB 121 TVYGGFYDECLRKRYGNANWKYFTDLFDYLPALTALIESQIFCLHGLSPS 2L 180
QY 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIAEQFNHTGL 2L 240
DB 181 DRIOEVPHGPMCDLLMSDDRCGWSISPRGAGYTFGODIAEQFNHTGL 2L 240
QY 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAP 2K 300
DB 241 VMEGYNMCDKXNVVTFSAFNVCYRCGNMAAIMEIDETNRSFLOPEAP 2K 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 4
Q9FSV3_FAGSY PRELIMINARY; PRT; 306 AA.
ID Q9FSV3_FAGSY PRELIMINARY; PRT; 306 AA.
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```
DR HSSP; P08129; 1FJM.  
DR InterPro: IPR004843; M-pestertase.  
DR InterPro: IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.  
DR PRINTS; PR00114; STPHPHASE.  
DR ProDom; PD000252; T.phrase_apah; 1.  
DR SMART; SM00156; PP2Ac; 1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.  
KM Hydroxylase; Iron; Manganese; Metal-binding; Multigene family;  
Protein phosphatase.  
KW ACT_SITE 115 115 Proton donor (By similarity).  
FT METAL 54 54 Iron (By similarity).  
FT METAL 56 56 Iron (By similarity).  
FT METAL 82 82 Iron and manganese (By similarity).  
FT METAL 114 114 Manganese (By similarity).  
FT METAL 164 164 Manganese (By similarity).  
FT METAL 238 238 Manganese (By similarity).  
SQ SEQUENCE 306 AA; 34934 MW; B2DCB1B3C2CD54F CRC64;  
Query Match 91.1%; Score 1522; DB 1; Length 306;  
Best Local Similarity 89.5%; Pred. No. 8 7e-127;  
Matches 274; Conservative 17; Mismatches 15; Indels 0; Gaps 0;  
QY 1 MESYADVDRQIEQLSECKPLSELEVNLCDOARTILVEEMVQPVKCPVTCGDHNGFH 60  
DB 1 MESNGDLDRQIEQLSECKPLSEADVRLCDQARALIVEEYNQPVKCPVTCGDHNGFY 60  
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRRLITLGNHESRQI 120  
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRRLITLGNHESRQI 120  
QY 121 TVGVGFYDECLARKYGANAVWKFTDLPDYLPPLTALIEHEIFCLHGLSPSLDTLDIRAL 180  
DB 121 TVGVGFYDECLARKYGANAVWKFTDLPDYLPPLTALIEHQVFCILHGLSPSLDTLDIRAL 180  
QY 181 DRIQEVPHGPMCDLLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTGLSLVARAHQL 240  
DB 181 DRIQEVPHGPMCDLLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTGLSLVARAHQL 240  
QY 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAALMEIDETMNRSLQEPAPRQSEPVYTK 300  
DB 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAALMEIDETMNRSLQEPAPRQSEPVYTK 300  
QY 301 TPDYFL 306  
DB 301 TPDYFL 306  
Db 301 TPDYFL 306  
RESULT 6  
Q9MB05 VICEA PRELIMINARY; PRT; 306 AA.  
ID Q9MB05 VICEA PRELIMINARY; PRT; 306 AA.  
AC Q9MB05;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Type 2A protein phosphatase-2.  
GN Name=vfpp2ac-2;  
OS Vicia faba (Broad bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
NCBI_TaxID=3906;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Ueno H., Kinoshita T., Aasanna M., Shimazaki K.,  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
phosphate.  
CC -1- Similarity: Belongs to the PPP phosphatase family.  
DR EMBL; AA039917; BAA32698.1; -; mRNA.  
DR HSSP; P36873; 1UK7.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR004843; M-pestertase.  
PR
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DR InterPro; IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.  
DR PRINTS; PR00114; STPHPHASE.  
DR ProDom; PD000252; T.phrase_apah; 1.  
DR SMART; SM00156; PP2Ac; 1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.  
KM Hydroxylase; Iron.  
SQ SEQUENCE 306 AA; 35008 MW; F9DAB0D2E872CC49 CRC64;  
Query Match 91.0%; Score 1519; DB 2; Length 306  
Best Local Similarity 89.9%; Pred. No. 1.6e-126;  
Matches 275; Conservative 16; Mismatches 15; Indels 0;  
QY 1 MESYADVDRQIEQLSECKPLSELEVNLCDOARTILVEEMVQPVKCPVT 60  
DB 1 MESQADLDRQIEHLMCKPLSEBVKALCDQARALIVEEMVQPVKCPVT 60  
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITTI 120  
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITTI 120  
QY 121 TVGVGFYDECLARKYGANAVWKFTDLPDYLPPLTALIEHEIFCLHGLSPS 180  
DB 121 TVGVGFYDECLARKYGANAVWKFTDLPDYLPPLTALIEHQVFCILHGLSPS 180  
QY 181 DRIQEVPHGPMCDLLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTNG 240  
DB 181 DRIQEVPHGPMCDLLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTNG 240  
QY 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAALMEIDETMNRSLQEPAP 300  
DB 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAALMEIDETMNRSLQEPAP 300  
QY 301 TPDYFL 306  
DB 301 TPDYFL 306  
Db 301 TPDYFL 306  
RESULT 7  
Q8LAW8 ARATH PRELIMINARY; PRT; 306 AA.  
ID Q8LAW8 ARATH PRELIMINARY; PRT; 306 AA.  
AC Q8LAW8;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Serine/threonine protein phosphatase type 2A, putative.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids  
NCBI_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
annotation";  
RL Genome Biol. 3:RESEAR0029-RESEAR0029(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.  
RA Feldmann K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
phosphate.  
CC -1- Similarity: Belongs to the PPP phosphatase family.  
DR EMBL; AY087557; AAM65099.1; -; mRNA.  
DR HSSP; P36873; 1ITE.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR004843; M-pestertase.  
DR InterPro; IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.
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DR PRINTS; PR00114; STPHPHASE.
DR ProDom; PD000252; T_phase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
DR Hydrolyase; Iron.
KW Hydrolyase; Iron.
SEQUENCE 306 AA; 34934 MW; 78699458192C1F08 CRC64;

Query Match 90.7%; Score 1514; DB 2; Length 306;
Best Local Similarity 89.2%; Pred. No. 4.5e-126;
Matches 273; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 MESYADVDRQIQSLSECKPLSELEVENLGDQARTILVEEMNQPVKCPVTGCDIHGQH 60
DB 1 MESNGDLDRQIQSLSECKPLSELEVENLGDQARTILVEEMNQPVKCPVTGCDIHGQH 60
QY 61 DLIELFRIGKAPDNTNLFMGDYVDRGYSVETVSLVALKVRDRITILKGNHESRQI 120
DB 61 DLIELFRIGKAPDNTNLFMGDYVDRGYSVETVSLVALKVRDRITILKGNHESRQI 120
QY 121 TVGVGYDECLRKYGNNANWKFTDLFDYLPPLTALIEHEIFCLHGLSPSLDTHIRAL 180
DB 121 TVGVGYDECLRKYGNNANWKFTDLFDYLPPLTALIEHEIFCLHGLSPSLDTHIRAL 180
QY 181 DRIQVPHGPMCDILMSDPDRCGMISPRGAGYTFGGDIAEOFNHTGSLVAAHQ 240
DB 181 DRIQVPHGPMCDILMSDPDRCGMISPRGAGYTFGGDIAEOFNHTGSLVAAHQ 240
QY 241 VMEGYNWCODKXNVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOPEAPROSEPTTRK 300
DB 241 VMEGYNWCODKXNVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOPEAPROSEPTTRK 300

QY 301 TPDPYFL 306
DB 301 TPDPYFL 306

RESULT 8
Q527K2_ORYSA PRELIMINARY; PRT; 306 AA.
ID Q527K2_ORYSA PRELIMINARY; PRT; 306 AA.
AC Q527K2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-1 catalytic subunit.
GN Name=OSUNBa0006A22.44;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacridae; Oryzaceae; Oryza.
NCBI_TaxID=39947;

OK NCBI_TaxID=39947;
RN NUCLEOTIDE SEQUENCE.
RP Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipoabare (GA3) genomic DNA, chromosome 6, BAC
RT clone:OSUNBa0006A22.44";
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
CC EMBL; AP004729; BAD61854.1; -; Genomic DNA.
DR Gramene; Q527K2;
DR GO; GO:0016787; P_hydrolyase activity; IEA.
DR InterPro; IPR004843; M-esterase.
DR InterPro; IPR006186; T_phase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPHASE.
DR ProDom; PD000252; T_phase_apah; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
DR Hydrolyase; Iron.
KW Hydrolyase; Iron.
SEQUENCE 306 AA; 35113 MW; F95722P8A638FF31 CRC64;
Query Match 90.5%; Score 1512; DB 2; Length 306;

Best Local Similarity 87.9%; Pred. No. 6.7e-126;
Matches 269; Conservative 25; Mismatches 12; Indels

QY 1 MESYADVDRQIQSLSECKPLSELEVENLGDQARTILVEEMNQPVKCPVT 60
DB 1 MESYADVDRQIQSLSECKPLSELEVENLGDQARTILVEEMNQPVKCPVT 60
QY 61 DLIELFRIGKAPDNTNLFMGDYVDRGYSVETVSLVALKVRDRITIL 120
DB 61 DLIELFRIGKAPDNTNLFMGDYVDRGYSVETVSLVALKVRDRITIL 120
QY 121 TVGVGYDECLRKYGNNANWKFTDLFDYLPPLTALIEHEIFCLHGLSP 180
DB 121 TVGVGYDECLRKYGNNANWKFTDLFDYLPPLTALIEHEIFCLHGLSP 180
QY 181 DRIQVPHGPMCDILMSDPDRCGMISPRGAGYTFGGDIAEOFNHTG 240
DB 181 DRIQVPHGPMCDILMSDPDRCGMISPRGAGYTFGGDIAEOFNHTG 240
QY 241 VMEGYNWCODKXNVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOPEAP 300
DB 241 VMEGYNWCODKXNVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOPEAP 300

QY 301 TPDPYFL 306
DB 301 TPDPYFL 306

RESULT 9
P2A_HEVER STANDARD; PRT; 306 AA.
ID P2A_HEVER STANDARD; PRT; 306 AA.
AC Q9ZSE4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A catalytic subunit
DE (EC 3.1.3.16).
GN Name=PP2A;
OS Hevea brasiliensis (Para rubber tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoide
OC Micrandeae; Hevea.
NCBI_TaxID=3981;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shin D.H., Han K.-H.;
RT "Isolation of a cDNA encoding a type 2A serine/threonine pr
RT phosphatase (PP2A) from Hevea brasiliensis.";
RL (er) Plant Gene Register PGR99-011.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
phosphate.
CC -1- CORACOR: Binds 1 iron ion per subunit (By similarity).
CC -1- CORACOR: Binds 1 manganese ion per subunit (By similar
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed at the same level in late
leaves.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2
subfamily.

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CC between the Swiss Institute of Bioinformatics and the EW
CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this e
removed.
CC EMBL; AF107464; AAD09953.1; -; mRNA.
DR HSSP; P08129; IFOM.
DR InterPro; IPR004843; M-esterase.
DR InterPro; IPR006186; T_phase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPHASE.
DR ProDom; PD000252; T_phase_apah; 1.

```
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolase; Iron; Manganese; Metal-binding; Multigene family;
KM Protein phosphatase.
FT ACT_SITE 115 115 Proton donor (By similarity).
FT METAL 54 54 Iron (By similarity).
FT METAL 56 56 Iron (By similarity).
FT METAL 82 82 Iron and manganese (By similarity).
FT METAL 114 114 Manganese (By similarity).
FT METAL 154 154 Manganese (By similarity).
FT METAL 238 238 Manganese (By similarity).
SQ SEQUENCE 306 AA; 34969 MW; EFBE7F9DFAEBA61 CRC64;

Query Match
Best Local Similarity 90.4%; Score 1509; DB 1; Length 306;
Matches 273; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MESSYADVDRQIQEQLSECKPLSELEVNKLCDAQRTILVEENWVQPVKCPVTCGDHIGQFH 60
DB 1 MESHGDLDRQIHLMECKPLPEARQGLCDQARAILVEENWVQPVKCPVTCGDHIGQFY 60
QY 61 DLIELFRIGKAPDPTNYLFMGDYVDGYYSVETVSLVALKVRKRRITILRGNHESROI 120
DB 61 DLIELFRIGKAPDPTNYLFMGDYVDGYYSVETVTLVALKVRKRRITILRGNHESROI 120
QY 121 TQVYGFYDECLRRKYGANWVKYFTDLPDYLPPLTALIEHEIFCLAGLSPLDTLHIRAL 180
DB 121 TQVYGFYDECLRRKYGANWVKYFTDLPDYLPPLTALIESQIFCLAGLSPLDTLHIRAL 180
QY 181 DRIQEVPHGPMCDLWSPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSIVARHQL 240
DB 181 DRIQEVPHGPMCDLWSPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLTISRHQL 240
QY 241 VMEGYNMCCQDNVTVTSAPNYCYRCGMAAIMEIDETMRSLSLOEPPAPROSEPRVTAK 300
DB 241 VMEGYNMCCQDNVTVTSAPNYCYRCGMAAILEIGENMAQNLQDPAPROIEPDTTK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 10
P2A3 ORYSA STANDARD; PRT; 307 AA.
ID P2A3 ORYSA 09XGT7;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-3 catalytic subunit
DE (EC 3.1.3.16).
GN Name=PP2A3;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_Taxid=4530;
OX RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Indica / IR36;
RA Yu R.M.K., Kong R.Y.C.;
RT Molecular cloning and characterization of protein phosphatase 2A
RT catalytic subunit genes from Oryza sativa."
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2A
CC subfamily.
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CC removed.
CC -----
CC EMBL; AF159061; AAD41126.1; -; Genomic_DNA.
CC DR HSSP; P08129; 1PTM.
CC DR Gramene; O9XGT7; -.
CC DR InterPro; IPR004843; M-esterase.
CC DR InterPro; IPR006186; T_phase_apah.
CC DR Pfam; PF00149; Metallophos; 1.
CC DR PRINTS; PR00114; STPHPHAS.
CC DR PRODOM; PD000252; T_phase_apah; 1.
CC DR SMART; SM00156; PP2Ac; 1.
CC DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolase; Iron; Manganese; Metal-binding; Multigene family
KM Protein phosphatase.
FT ACT_SITE 116 116 Proton donor (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 57 57 Iron (By similarity).
FT METAL 83 83 Iron and manganese (By similar
FT METAL 115 115 Manganese (By similarity).
FT METAL 165 165 Manganese (By similarity).
FT METAL 239 239 Manganese (By similarity).
SQ SEQUENCE 307 AA; 35145 MW; 97143563695D0D6 CRC64;

Query Match
Best Local Similarity 90.3%; Score 1508.5; DB 1; Length 3
Matches 272; Conservative 23; Mismatches 11; Indels 1;

QY 1 MESSYADVDRQIQEQLSECKPLSELEVNKLCDAQRTILVEENWVQPVKCPV 59
DB 1 MESHGDLDRQIAQRECHLAEGEVRLCEQAKAILVEENWVQPVRCV 60
QY 60 HDLIELFRIGKAPDPTNYLFMGDYVDGYYSVETVSLVALKVRKRRDRT 119
DB 61 YDLIELFRIGKAPDPTNYLFMGDYVDGYYSVETVSLVALKVRKRRDRT 120
QY 120 ITQVYGFYDECLRRKYGANWVKYFTDLPDYLPPLTALIEHEIFCLAGLSPL 179
DB 121 ITQVYGFYDECLRRKYGANWVKYFTDLPDYLPPLTALIEHQVCLAGLSPL 180
QY 180 LDRIQEVPHGPMCDLWSPDDRCGNGISPRGAGYTFGQDIAEQFNHTN 239
DB 181 LDRIQEVPHGPMCDLWSPDDRCGNGISPRGAGYTFGQDIAEQFNHTN 240
QY 240 LYMEGYNMCCQDNVTVTSAPNYCYRCGMAAIMEIDETMRSLSLOEPPA 299
DB 241 LYMEGYNMCCQDNVTVTSAPNYCYRCGMAAILEIGENMDQNLQDPAP 300
QY 300 KTPDYFL 306
DB 301 KTPDYFL 307

RESULT 11
Q6Z6L9 ORYSA PRELIMINARY; PRT; 307 AA.
ID Q6Z6L9;
AC 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-3 catalytic subun
GN Name=P0027A02.2-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
OX RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
 CC EMBL, AF004996; BAD1714.1; -, Genomic_DNA.
 CC HSSP, Q08209; 1AU1.
 DR Gramene; Q62619; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR004843; M-esterase.
 DR InterPro; IPR006186; T_phatase_apah.
 DR Pfam; PF00149; Metallophos; 1.
 DR PRINTS; PR00114; STPHPHASE.
 DR ProDom; PD000252; T_phatase_apah; 1.
 DR SMART; SM00156; PP2Ac; 1.
 DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
 DR Hydrolase; Iron.
 SQ SEQUENCE 307 AA; 35144 MW; 97143563695D0DD6 CRC64;
 Query Match 90.3%; Score 1508.5; DB 2; Length 307;
 Best Local Similarity 88.6%; Pred. No. 1.4e-125;
 Matches 272; Conservative 23; Mismatches 11; Indels 1; Gaps 1;

QY 1 ME-SYADVADROIEQISECKPLSELEVKMLCDQARTLLVEENVQPYKCPVTGDIHQGF 59
 DB 1 MESSHGDLDROIAQLRECGHLEGEVRAICBOAKMIMEWVQPRCPVTGDIHQGF 60
 QY 60 HLLIEFRIGGAPDTNLYFMGDYDRGYSVETVSLVALKVRTRDTITLRGNHESRQ 119
 DB 61 YLIEIFRIGGAPDTNLYFMGDYDRGYSVETVSLVALKVRTRDTITLRGNHESRQ 120
 QY 120 IYQVGFYDECRKTKGNANVMKFTDLPYLPLTALIEHIFCLGQSPSLDTLDHTR 179
 DB 121 ITQVGFYDECRKTKGNANVMKFTDLPYLPLTALIEHIFCLGQSPSLDTLDHTR 180
 QY 180 LDRIGVEPHEGPMCDLMSDPDRCGWGISPRGAGYTFGQDIAEOPFNTNGSLVARAQ 239
 DB 181 LDRIGVEPHEGPMCDLMSDPDRCGWGISPRGAGYTFGQDIAEOPFNTNGSLVARAQ 240
 QY 240 LVMEGYNNQODKXVTVTFSAFNYCYRCGNMAIMEIDFNMSFLQEPAPQSEPDVTR 299
 DB 241 LVMEGYNNQODKXVTVTFSAFNYCYRCGNMAIMEIDFNMSFLQEPAPQSEPDVTR 300
 QY 300 KTPDYFL 306
 DB 301 KTPDYFL 307

RESULT 12
 P2A2 ARATH STANDARD; PRT; 306 AA.
 AC 007099;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Serine/threonine protein phosphatase PP2A-2 catalytic subunit (EC 3.1.3.16).
 OS Name=PP2A2; OrderedLocustNames=At1G59830; ORENames=F23H11.15;
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxId=3702;
 RX NUCLEOTIDE SEQUENCE.
 RP STRAIN=cv. Columbia GUL;
 RX MEDLINE=93184204; PubMed=8382968;
 RA Arino J., Perez-Callejon E., Cunillera N., Camps M., Posas F.,
 RA "Protein phosphatases in higher plants: multiplicity of type 2A
 RT phosphatases in Arabidopsis thaliana".
 RL Plant Mol. Biol. 21:475-485(1993).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federpiel N.A., Kaul
 RA White O., Alonso J., Alatafi H., Araujo R., Bowman C.L., Bec
 RA Bueller E., Chan A., Chao Q., Chen H., Cheuk R.P., Chin C.K
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki
 RA Kim C.T., Koo H.L., Kremetska I., Kurtz D.B., Kwan A.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Marzall
 RA Miltseher J., Miranda M., Nguyen M., Nierman W.C., Osborne
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southc
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utecherback T., Van Aken S., Vayberg M., Vysotskaia V.S., Wa
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabid
 RL thaliana".
 RT Nature 408:816-820(2000).
 RN (3)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1086
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cf
 RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toz
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K.,
 RA Arakawa T., Banh J., Banno F., Bowser S.Y., Carr
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hanse
 RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Kai
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sa
 RA Saitou M., Tamse R., Vayberg M., Wallender E.K., Wong C., Y
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.
 RT "Empirical analysis of transcriptional activity in the Arab
 genome.";
 RT Science 302:842-846(2003).
 RL -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
 CC phosphate.
 CC -1- COPACITOR: Binds 1 iron ion per subunit (By similarity).
 CC -1- CORACITOR: Binds 1 manganese ion per subunit (By similar
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2
 CC subfamily.
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 CC -----
 DR EMBL, M96732; AAA32847.1; -, mRNA.
 DR EMBL, AC007258; AAD39326.1; -, Genomic_DNA.
 DR EMBL, AY063942; AAL36298.1; -, mRNA.
 DR EMBL, AY096543; AAM20193.1; -, mRNA.
 DR PIR, S31161; S31161.
 DR HSSP; P36873; 1176.
 DR InterPro; IPR004843; M-esterase.
 DR InterPro; IPR006186; T_phatase_apah.
 DR Pfam; PF00149; Metallophos; 1.
 DR PRINTS; PR00114; STPHPHASE.
 DR ProDom; PD000252; T_phatase_apah; 1.
 DR SMART; SM00156; PP2Ac; 1.
 DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 DR Hydrolase; Iron; Manganese; Metal-binding; Multigene family
 KM Protein phosphatase.
 KW ACT_SITE 115 115
 FT METAL 54 54 Proton donor (By similarity).
 FT METAL 56 56 Iron (By similarity).
 FT METAL 82 82 Iron and manganese (By similar
 FT METAL 114 114 Manganese (By similarity).

FT	METAL	164	164	Manganese (By similarity).
FT	METAL	238	238	Manganese (By similarity).
SQ	SEQUENCE	306 AA;	34961 MW;	579427029db41a1c1 CRC64.
Query Match 90.3%; Score 1508; DB 1; Length 306;				
Best Local Similarity 88.9%; Pred. No. 1,5e-125;				
Matches 272; Conservative 17; Mismatches 17; Indels 0; Gaps 0;				
QY	1	MPSYADVDRQIEQLSECKPLSELEKVNLCDOARTILVEEMVQPVKCPVYCGDIHGQFH	60	
Db	1	MLPLNGDIDRQIEQLSECKPLSEADVKILCDQAKALIVEENVQPVKCPVYCGDIHGQFY	60	
QY	61	DLILFLRIGGAAPDTNTYLFMGDYDRGRYSVETVSLVALKRYRDRITTLIRGNHESQI	120	
Db	61	DLILFLRIGGAAPDTNTYLFMGDYDRGRYSVETVSLVALKRYRDRITTLIRGNHESQI	120	
QY	121	TQVYGFPEDECRRKIGNANVMKFFDLPYLLPTALIEHIFCLHGSLSPSLDTHIRAL	180	
Db	121	TQVYGFPEDECRRKIGNANVMKFFDLPYLLPTALIEHIFCLHGSLSPSLDTHIRAL	180	
QY	181	DRIGVEPHEGMC DLLMSDPDRCGWGISPRGAGYTFGODIAEONHTNGISLVARAQL	240	
Db	181	DRIGVEPHEGMC DLLMSDPDRCGWGISPRGAGYTFGODIAEONHTNGISLVARAQL	240	
QY	241	VMEGYNNCODKNVTVTFSPAPNYCYRCGMAALMEIDETMNSFLQEPAPROSEPDYTRK	300	
Db	241	VMEGYNNCODKNVTVTFSPAPNYCYRCGMAALMEIDETMNSFLQEPAPROSEPDYTRK	300	
QY	301	TPDYFL 306		
Db	301	TPDYFL 306		
RESULT 13				
ID	P2A1_ORYSA	STANDARD:	PRT;	306 AA.
AC	Q9ZSS3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Serine/threonine protein phosphatase Pp2A-1 catalytic subunit (EC 3.1.3.16).			
GN	Name=PP2A1;			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Erbartoideae; Oryzaceae; Oryza.			
OX	NCBI_TaxID=4530;			
RN	[1]			
RP	NCBIOTIDE SEQUENCE.			
RC	STRAIN=cv. Indica / IR36;			
RA	Yu R.M.K., Zhou Y., Xu P., Kong R.Y.C.;			
RT	"Isolation and characterization of a rice gene encoding a catalytic subunit of protein phosphatase 2A.";			
RT	Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.			
CC	-1- COFACTOR: Binds 1 iron ion per subunit (By similarity).			
CC	-1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-1- SIMILARITY: Belongs to the ppp phosphatase family. pp-2A subfamily.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
DR	EMBL; AF097182; AAC72838.1; -; Genomic_DNA.			
DR	HSSP; P08129; 1F7M.			
DR	Gramene; Q9ZSS3; -;			
DR	InterPro; IPR003493; M-pestasease.			

DR	InterPro: IPR006186; T_phcAse_apah.
DR	Pfam; PF00149; Metallophos_1.
DR	PRINTS; PR00114; STEPHATASE.
DR	ProDom; PD000252; T_phcAse_apah; 1.
DR	SMART; SMO0156; Pp2Ac; 1.
DR	PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KM	Hydrolase; Iron; Manganese; Metal-binding; Multigene family
KW	Protein phosphatase.
FT	ACT_SITE 115 115 Proton donor (By similarity).
FT	METAL 54 54 Iron (By similarity).
FT	METAL 56 56 Iron (By similarity).
FT	METAL 82 82 Iron and manganese (By similar
FT	METAL 114 114 Manganese (By similarity).
FT	METAL 164 164 Manganese (By similarity).
FT	METAL 238 238 Manganese (By similarity).
SQ	SEQUENCE 306 AA; 35128 MW; 5DC7F99510E272F9 CRC64;
Query Match	Best Local Similarity 90.2%; Score 1506; DB 1; Length 306 Matches 268; Conservative 25; Mismatches 13; Indels
Qy	1 MPSYADVDRQIEQLSECKPLSELEVKMLCDARITLVEKNVOPKCEVT
Dz	1 MPSSADLDROISQRECKFLGEAVRALCEDAKALIMEKNVQPRCVYT
Qy	61 DLIELFRIGKAPDTNTYLEMGDIYDGRYSYEVTSLVALKVRIRDRITTI
Dz	61 DLIELFRIGDSPTNTNLFEMGDYVDGRYSYEIVTLLVALKYRIRDRITTI
Qy	121 TOYVGFDDECLRKKGNNVMWKYPFDLPPLYELTLIHEIFCLHGLSPS
Dz	121 TOYVGFDDECLRKGNNVMWKYPFDLPPLYELTLIHEIFCLHGLSPS
Qy	181 DRIGEVPHGEGMCULLMSDDPDRCGMGISPPGAGTYFEQDLADEFNHNG
Dz	181 DRIGEVPHGEGMCULLMSDDPDRCGMGISPPGAGTYFEQDLADEFNHNG
Qy	241 VMEGFNMCCQDKNVTVFSAPNYCYRCGNMAAMEIDETMNSFLQFBAP
Dz	241 VMEGFNMCCQDKNVTVFSAPNYCYRCGNMAALEIGENMDNFLQFBAP
Qy	301 TEDYFL 306
Dz	301 TEDYFL 306
RESULT 14	
ID_P2A_HELAN	STANDARD; PRT; 305 AA.
AC	P48579;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Serine/threonine protein phosphatase Pf2A catalytic subunit (EC 3.1.3.16).
OS	Helianthus annuus (Common sunflower).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo-
OC	spermatophytes; Magnoliophyta; eudicotyledons; core eudicoty
OC	asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC	Heliantheae; Helianthus.
OX	NCBI_TaxID=4232;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Root meristem;
RX	MEDLINE=9539397; PubMed=7664759;
RA	Wenzel D., Vugrek O., Frank S., Eisner-Wenzel C.,
RT	"Protein phosphatase 2A, a potential regulator of actin dyn
RL	Eur. J. Cell Biol. 67:179-187(1995).
CC	-1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC	n phosphate.
CC	-1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC	-1- COFACTOR: Binds 1 manganese ion per subunit (By simil

CC -1- SIMILARITY: Belongs to the PPP phosphatase family. pp-2A
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z26041; CAA61126.1; -, mRNA.
CC PIR; S37086; S37086.
CC HSSP; P08129; 1FWM.
CC InterPro; IPR004843; M-esterase.
CC InterPro; IPR006186; T_phatase_apah.
CC Pfam; PF00149; Metallophos; 1.
CC PRINTS; PR00114; STRPHRASE.
CC ProDom; PD000252; T_phatase_apah; 1.
CC SMART; SM00156; PP2Ac; 1.
CC PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
CC Hydrolyase; Iron; Manganese; Metal-binding; Multigene family;
CC Protein phosphatase.
CC ACT SITE 114 114 Proton donor (By similarity).
FT METAL 53 53 Iron (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 81 81 Iron and manganese (By similarity).
FT METAL 113 113 Manganese (By similarity).
FT METAL 163 163 Manganese (By similarity).
FT METAL 237 237 Manganese (By similarity).
SQ SEQUENCE 305 AA; 34865 MW; 0B9D14F3DD0B950 CRC64;

Query Match 89.9%; Score 1501.5; DB 1; Length 305;
Best Local Similarity 88.2%; Pred. No. 5.8e-125;
Matches 270; Conservative 21; Mismatches 14; Indels 1; Gaps 1;

QY 1 MSYADVDRQIQSLSECKPLSELEVNKLCDOARTILVEEMNVPYKCPVTCGDIHGQF 60
DB 1 MESQSDLDQIHLMDCKLPE-EVRTLCDQARTILVEEMNVPYKCPVTCGDIHGQF 59
QY 61 DLIELFRIGKAPDNTYLFMGDYVDRGYSVETSLVLVALKVRDRITILGNHESRQI 120
DB 60 DLIELFRIGSAPDNTYLFMGDYVDRGYSVETSLVLVALKVRDRITILGNHESRQI 119
QY 121 TQVYGFYDECLAKKYGNAWVKYFTDLFDYLPFTALIEHIFCLHGLSGSLDTLHTRAL 180
DB 120 TQVYGFYDECLAKKYGNAWVKYFTDLFDYLPFTALIEHIFCLHGLSGSLDTLHTRAL 179
QY 181 DRIOEVPHGPMCDLLSPDDRCGMSIPRGAGYFFGQDIAEOPHTNGLSIVARHQL 240
DB 180 DRIOEVPHGPMCDLLSPDDRCGMSIPRGAGYFFGQDIAEOPHTNGLSIVARHQL 239
QY 241 VMEGYNMCDKXNVTVFSAPNYCYRCGNAAIMEIDETNRSFLQEPAPROSEPDVTRK 300
DB 240 VMEGYNMCDKXNVTVFSAPNYCYRCGNAAIMEIDETNRSFLQEPAPROSEPDVTRK 299
QY 301 TPDYFL 306
DB 300 TPDYFL 305

RESULT 15
P2A5_ARATH STANDARD; PRT; 307 AA.
ID_P2A5_ARATH Q42544; Rel. 40; Created
AC 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DR 13-SEP-2005 (Rel. 48; Last annotation update)
DE Serine/threonine protein phosphatase PP2A-5 catalytic subunit
(EC 3.1.3.16)
GN Name=P2A5; OrderedLocustNames=At1g69960; ORFNames=F2095.30, T1773.1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Columbia;
RA Stamey R.T., Rundle S.J.;
RT "Characterization of a novel isoform of a type 2A serine/th
RT protein phosphatase from Arabidopsis thaliana";
RL (ex) Plant Gene Register PCR95-116.
RN [2]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Becker J.R., Palm C.U., Federspiel N.A., Kaul
RA White O., Alonso J., Alcafi H., Araujo R., Bowman C.L., Bc
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressey T.H.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fuji
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki
RA Kim C.U., Koo H.L., Kremenevskaya I., Kurtz D.B., Kwan A.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani
RA Miltoscher J., Miranda M., Nguyen M., Nierman W.C., Osborne
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwic
RA Sun H., Tallon L.J., Tambunga G., Tortum L.J., Town C.D.,
RA Utecherback T., Van Aken S., Vayenberg M., Vayotskaya V.S., Wa
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabid
RT thaliana";
RL Nature 408:816-820(2000).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC phosphatase.
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similar
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. pp-2
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMB
CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this s
CC removed.
CC -----
CC EMBL; U39568; AAC668.1; -, mRNA.
CC EMBL; AC002062; AAB6116.1; -, Genomic DNA.
CC EMBL; AC010675; AAG52565.1; -, Genomic DNA.
CC PIR; B96722; B96722.
CC HSSP; P36873; 11T6.
CC InterPro; IPR004843; M-esterase.
CC InterPro; IPR006186; T_phatase_apah.
CC Pfam; PF00149; Metallophos; 1.
CC PRINTS; PR00114; STRPHRASE.
CC ProDom; PD000252; T_phatase_apah; 1.
CC SMART; SM00156; PP2Ac; 1.
CC PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
CC Hydrolyase; Iron; Manganese; Metal-binding; Multigene family
KW Protein phosphatase.
FT ACT SITE 116 116 Proton donor (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 57 57 Iron (By similarity).
FT METAL 83 83 Iron and manganese (By similar
FT METAL 115 115 Manganese (By similarity).
FT METAL 165 165 Manganese (By similarity).
FT METAL 239 239 Manganese (By similarity).
SQ SEQUENCE 307 AA; 35042 MW; D00149EAOE20C82F CRC64;

Query Match 89.5%; Score 1495; DB 1; Length 307
Best Local Similarity 87.9%; Pred. No. 2.2e-124;
Matches 268; Conservative 23; Mismatches 14; Indels

Db	3	PATGDI DRQIEQMECKALSETEVKMLCEHAKTILVEEYNQPVKCPVTVCGBDIGHQFYD	62
Qy	62	LIELFRIGKAPDTNTYLFMGDYVDRCGYSEVETVSLVALKVRXRDRITILRGNHESRQIT	121
Db	63	LIELFRIGSSPDTNTYLFMGDYVDRCGYSEVETVSLVALKVRXRDRITILRGNHESRQIT	122
Qy	122	QYVGFYDECLRKYGNNANVWKYFTDLFDYLPALTALIEHIFCLHGLSPSLDTLDHIRALD	181
Db	123	QYVGFYDECLRKYGNNANVWKHFTDLPALTALIESQVFCILHGLSPSLDTLDNIRSLD	182
Qy	182	RIQEVPHEGPMCDLMSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSIVARAHQLY	241
Db	183	RIQEVPHEGPMCDLMSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSISRAHQLY	242
Qy	242	MEGYNNCQDKNTVTVFSAPNYCYRCGNMAIMEIDETNRSFLQEPAPROSEPDVTRKT	301
Db	243	MEGFNWCQEKNTVTVFSAPNYCYRCGNMAILIEIGENMDQNFLOFDPAPROVEPETTRKT	302
Qy	302	PDYFL 306	
Db	303	PDYFL 307	

Search completed: December 9, 2005, 10:23:18
Job time : 165 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:24:12 ; Search time 4445 Seconds
(without alignments)
3913.182 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MPYADVDRQIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QWMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10764259 @CEN 1.1 7415 @runat_05122005_094547_7015 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

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10: gb.sts.*

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14: gb.htg.*

15: gb.pl.*

SUMMARIES

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1	1670	100.0	1365	6	AR606281 Sequence
2	1670	100.0	1365	6	AX490719 Sequence
3	1548	92.7	1511	15	AY325818 Lycopersi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4	1538	92.1	1417	15	AB039916	AB03
5	1534	91.9	1380	15	AY325817	AY32
6	1526	91.4	1497	15	FSY298829	AY29
7	1522	91.1	1092	15	AY093267	AY09
8	1522	91.1	1264	15	ATHPRPHB	M967
9	1522	91.1	1343	15	AY059847	AY05
10	1519	91.0	1475	15	AB039917	AB03
11	1514	90.7	1261	15	AY087557	AY08
12	1509	90.4	1370	15	AF107464	AF10
13	1508.5	90.3	1563	15	AK072676	AK07
14	1508	90.3	921	6	AX506010	AX506
15	1508	90.3	952	15	AY096543	AY09
16	1508	90.3	1256	15	ATHPRPHA	M967
17	1508	90.3	1288	15	AY063942	AY06
18	1501.5	89.9	1211	15	HAPRPH2A	Z260
19	1495	89.5	924	6	AX505876	AX505
20	1495	89.5	1238	15	ATU39568	U395
21	1488	89.1	1376	15	AK071838	AK07
22	1481	88.7	1747	15	OSU49113	U491
23	1445	86.5	1708	15	NTNPP4	Z937
24	1440.5	86.3	1545	15	BT014167	BT01
25	1427	85.4	930	9	MMPHO2A1A	Z6774
26	1427	85.4	930	11	AY892088	AY89
27	1427	85.4	930	11	BT007581	BT00
28	1427	85.4	1617	4	BT021727	BT021
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31	1427	85.4	1771	4	BTFP2A	X7285
32	1427	85.4	1787	6	AR266601	AR266
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34	1427	85.4	1793	9	BC070914	BC070
35	1427	85.4	1804	6	AX401948	AX401
36	1427	85.4	1804	9	BC003856	BC003
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40	1427	85.4	1814	9	BC054458	BC054
41	1427	85.4	1820	8	BC031696	BC031
42	1427	85.4	1824	8	BC000400	sapi
43	1427	85.4	1824	8	BC019275	BC019
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45	1427	85.4	1839	8	AB169507	AB169

ALIGNMENTS

RESULT 1	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
LOCUS	AR606281					
DEFINITION	AR606281					
ACCESSION	AR606281.1	GI:56658183				
VERSION	Unknown.					
KEYWORDS	Unknown.					
SOURCE	Unclassified.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1365)					
AUTHORS	da Costa e Silva,O., Bohnert,H.J., van Thielen,N., C					
TITLE	Phosphatase stress-related proteins and methods of u					
JOURNAL	Patent: US 6818805-A 8 16-NOV-2004;					
FEATURES	BASF Plant Science GmbH; Ludwigshafen;					
source	DEX;					
Location/Qualifiers	1..1365					
/organism="unknown"	/mol_type="genomic DNA"					
ORIGIN						
Alignment Scores:						
Pred. No.:	1.59e-160					1365
Score:	1670.00					Matches: 306
Percent Similarity:	100.00%					Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x AR606281 (1-1365)

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DB 71 ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGCGAGGTGCAAGCGGTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaAtrGThrIleLeuValGluGluTrp 40
DB 131 TCGAGTTGGAGGTGAGAACCTATGTATCAAGCTCGAGCCGATCTTGGTGGAGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 191 AACGTGCAGCCGTAAGTGTCTGTACGGTTTCGGGTGACATCCATGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrIleuPheMet 80
DB 251 GATCTCATCGAGCTTTTCGCATAGAGGCAAGCGCCGACACCAACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
DB 311 GCGGACTATGTGAGTGTGATATTTCTGTGAGACTGTGTGCTCTTATGTGSCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 371 AAGGTGCGGTATAGGATAGGATCAATCTTTCGAGGGAACCCAGAGAGGAGGAT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 431 AGCGAAGTATATGGTTTCTATGATGAATGCTCGGGAAGTATGGAATCGAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 491 AAGTACTTCACGATCTGTTCACCTACCTGCTCTGACAGCTCTCATTTGAGGACAGAT 550
QY 161 PheCysLeuHisGlyLysLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 551 TTTTGTCTTCATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACAATCCGAGCCCTA 610
QY 181 AspArgIleGlnValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 611 GATCGTATTTCAAGAGTGCACGAGGCGCCGATGTGTGATCTACTCTGTCTGATCCA 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 671 GATGATCGTTGTGGATGGGGCAATTCACCAAGGTGCGGTTATATCTTTTGGTCAAGAT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 731 ATTGCAGACAGTTCAATCATACCAATGTTTAAAGTTTGGTTCAGTCTCACCAGCTT 790
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
DB 791 GTGATGGAAGGATACAAATTTGGTGCCAGGATAAAATGTTGTACAGTTTTCAGTCCCCC 850
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
DB 851 AATTACTGTACCGCTGTGGACATGCGCGCCATATGAGATAGATGAACAATGAT 910
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
DB 911 CGGTCTTTTCTTCAGTTTCAAGACCAAGCAGCCGCGCAAGTGAACAGATGTGACGCGGAAG 970
QY 301 ThrProAspTyrPheLeu 306
DB 971 ACTCCTGATTACTTTCTG 988
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RESULT 2
AX490719
LOCUS AX490719 1365 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 8 from Patent WO0246442.
ACCESSION AX490719
VERSION AX490719.1 GI:22323691
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Phys;
da Costa,E.S., Bohnert,H.J., Ishitani,M., van Thiele
Chan,R.
Phosphatase stress-related proteins and methods of u
Patent: WO 0246442-A 8 13-JUN-2002;
JOURNAL BASF Plant Science GmbH (DE)
FEATURES
source
1. 1365
/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN

Alignment Scores:
Pred. No.: 1598-160 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x AX490719 (1-1365)

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QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCys 20
DB 71 ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTCGAGGTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaAtrGThrIleLeuVal 40
DB 131 TCGGAGTTGGAGGTGGAAGAACCTATGTATCAAGCTCGAGCGATCTTGGT 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
DB 191 AACGTGCAGCCGTAAGTGTCTGTACGGTTTCGGGTGACATCCATGG 250
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyr 80
DB 251 GATCTCATCGAGCTTTTCGCATAGAGGCAAGCGCCGACACCAACTA 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 311 GCGGACTATGTGGATCGTGGATATTAATCTGTGAGAGCTGTGTGCTCTT 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120
DB 371 AAGGTGCGGTATAGGATAGGATCAATCTTCGAGGGAACCCAGAGAG 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
DB 431 AGCGAAGTATATGGTTCATGATGAATGCTCGGGAAGTATGGAATGCA 490
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGlu 160
DB 491 AAGTACTTCACGATCTGTTCGACTACCTGCTCTGACAGCTCTCATTTG 550
QY 161 PheCysLeuHisGlyLysLeuSerProSerLeuAspThrLeuAspHisIle 180
DB 551 TTTTGTCTTCATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACA 610
QY 181 AspArgIleGlnValProHisGluGlyProMetCysAspLeuLeuTrp 200
DB 611 GATCGTATTTCAAGAGTGCACGAGGCGCCGATGTGTGATCTACTCTGT 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPhe 220
DB 671 GATGATCGTTGTGGATGGGGCAATTCACCAAGGTGCGGTTATATCTTT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla 240
DB 731 ATTGCAGACAGTTCAATCATACCAATGTTTAAAGTTTGGTTCAGTCTCA 790
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhe 260
DB 791 GTGATGGAAGGATACAAATTTGGTGCCAGGATAAAATGTTGTACAGTT 850
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG 280
DB 851 AATTACTGTACCGCTGTGGACATGCGCGCCATATGAGATAGATGAACA 910
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300
DB 911 CGGTCTTTTCTTCAGTTTCAAGACCAAGCAGCCGCGCAAGTGAACAG 970
QY 301 ThrProAspTyrPheLeu 306
DB 971 ACTCCTGATTACTTTCTG 988
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RESULT 2
AX490719
LOCUS

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Db      671  GATGATCGTTGTGGATGGGCAATTTCCACCAGGATGCGGTTATATCTTTTGGTCAAGAT 730
Qy      221  ileAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db      731  ATTGCAGAGCAGTTCAATACCAATAGGTCTAAGTTTGGTTGCACGTGCTCACCAGCTT 790
Qy      241  ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db      791  GTGATGGAAGGATACAATTTGGTGCAGGATAAAATGTTGTCCACAGTTTTCAGTCCGCC 850
Qy      261  AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
Db      851  AATTAATGTTTACCGCTGTGGAAACATGCGCCGCAATAATGGAGATAGATGAACAATGAAT 910
Qy      281  ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db      911  CGGTCTTTCTTCAGTTTGAACAGCAGCCGCGGCAAGTAGAACCAAGATGTGACGGCGAAG 970
Qy      301  ThrProAspTyrPheLeu 306
Db      971  ACTCCTGATTACTTCTG 988

RESULT 3
AY325818      1511 bp      mRNA      linear      PLN 05-MAY-2004
LOCUS      Lycopersicon esculentum protein phosphatase 2A catalytic subunit
DEFINITION      (PP2Ac2) mRNA, complete cds.
ACCESSION      AY325818
VERSION      AY325818.1  GI:34398262
KEYWORDS      Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM      Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1511)
He,X., Anderson,J.C., Pozo Od.O., Gu,Y.Q., Tang,X. and Martin,G.B.
Silencing of subfamily I of protein phosphatase 2A catalytic
subunits results in activation of plant defense responses and
localized cell death
Plant J. 38 (4), 563-577 (2004)
JOURNAL
PUBMED      15125764
REFERENCE      2 (bases 1 to 1511)
AUTHORS      He,X., Anderson,J.C., del Pozo,O., Gu,Y.-Q., Tang,X. and
Martin,G.B.
TITLE      Direct Submission
JOURNAL      Submitted (18-JUN-2003) Boyce Thompson Institute, Cornell
University, Tower Road, Ithaca, NY 14853, USA
FEATURES
source
1..1511
/organism="Lycopersicon esculentum"
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/cultivar="OS4"
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1..1511
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1..306
/gene="pp2Ac2"
307..1227
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FCLHGLSPSLDNLNIALDRLOEPHPEGPMCDLWSDPDDRCMGWISPRGAGYTFG
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ORIGIN
Alignment Scores:
Pred. No.:      5,28-148
Score:          1548.00
Length:         1511
Matches:        279
Conservative:   15
Percent Similarity: 96.08%
Best Local Similarity: 91.18%
Mismatch:       12
Query Match:    92.69%
Indels:         0
Gaps:          0
DB:            15

US-10-764-259-13 (1-306) x AY325818 (1-1511)
Qy      1  MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys 20
Db      307  ATGCCGCTCATGCAGATCTAGATCGGCAGATCGAACAATTCATGCGAGTG 366
Qy      21  SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
Db      367  TCGGAAGCTGATGTGAATAACTCTGTGTGATCAAGCGAGGGCTATACTTGT 426
Qy      41  AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln 60
Db      427  AATGTTCAACCGGTGAATGTCCGGTGACTGTTTGTGGTGATATTCATGG 486
Qy      61  AspLeuIleGluLeuPheArgIleGlyCysLysAlaProAspThrAsnTyr 80
Db      487  GACCTGATTGAGCTGTTTCGGATTGGAGAAATGCTCCTGATACTAATTA 546
Qy      81  GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe 100
Db      547  GCGGATTATGTTGACCGGTGACTATTTCAGTGAGACTGTCCACACTTTT 606
Qy      101  LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120
Db      607  AAGGTTCTGTATAGATAGATAGAAATCAGATTCTTAGGGGAATCATGAAG 666
Qy      121  ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 140
Db      667  ACCCAAGTGTATGTTTTTATGATGAATGCTTGGAGAAATATGGCAATGC 726
Qy      141  LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGl 160
Db      727  AAGTATTTCACTGATCTTTTGTATCTATCCACTAACAGCACTGATAGA 786
Qy      161  PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIl 180
Db      787  TTCGTTTGGCAAGGAGACTCTCACCCTCTCTGGATACACTGGATAATAT 846
Qy      181  AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr 200
Db      847  GACCGTATACAAGAGGTTCCACATGAAGGGCCAATGTGTGATCTCCTGTG 906
Qy      201  AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh 220
Db      907  GATGATCGTGTGGTTGGGAAATCTCACCCTCGAGGGGCTGGTTATACCTI 966
Qy      221  IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240
Db      967  ATAGACTCTCAATTCATACCAATGCTCAGGATAAAGATGTTGTGACAGTAT 1026
Qy      241  ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh 260
Db      1027  GTGATGGAGGGTTTCAATTTGGTGTGTCAGGATAAAGATGTTGTGACAGTAT 1086
Qy      261  AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl 280
Db      1087  AACTATTGTTACCGGTGTGGTAAATATGGCTGCCATTCTAGAAATAGGCGA 1146
Qy      281  ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa 300
Db      1147  CAGAAATTCCTTCAGTTTGGCCAGCTCCTCGACAGATAGAGCCCGACAC 1206
Qy      301  ThrProAspTyrPheLeu 306

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Db 1207 ACTCCAGATTACTTTTGG 1224

RESULT 4

AB039916

LOCUS

DEFINITION

AB039916 1417 bp mRNA linear PLN 15-MAR-2000

Vicia faba vFPP2AC-1 mRNA for type 2A protein phosphatase-1, complete cds.

ACCESSION

AB039916

VERSION

vFPP2AC-1 GI:7248358

KEYWORDS

2 (bases 1 to 1417)

SOURCE

Vicia faba (fava bean)

ORGANISM

Vicia faba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.

REFERENCE

1 (bases 1 to 1417)

AUTHORS

Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.

TITLE

Type 2A protein phosphatase from guard cells of Vicia faba

JOURNAL

Published Only in DataBase (2000)

REFERENCE

2 (bases 1 to 1417)

AUTHORS

Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.

TITLE

Direct Submission

JOURNAL

Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu University, Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka 810-8560, Japan (E-mail: toshinori@box.nc.kyushu-u.ac.jp, Tel:81-92-726-4763 (ex.4763), Fax:81-92-726-4644)

FEATURES

Location/Qualifiers

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/organism="Vicia faba"

/mol_type="mRNA"

/db_xref="taxon:3906"

/cell_type="guard cell protoplasts"

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/note="synonym:Vicia faba L."

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256..1176

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/protein_id="BA092697.1"

/db_xref="GI:7248359"

/translation="MPSHADLDROIHELMCKPLPADVKALCDQARAILVEEMVQPVKCPVTVCDDIHGFYDIIELEFIGNAPDTNLFMGDYVDRGYSVETSLILVAKVRYRDRITILRGHESRQITQVYGFVDECLRYGNANWKFFTDLFDYLPALTALIESQIFCLHGLSLDNLRIALDRIOVPHGPMCDLLWSDPDDRCGWSIPRGAGYTFQDIAQPHNTGLSLISRAHQLVMEGYNWCQEKVVTVPFAPNYCYRCGNMAILIEIGENWQNFQDFPAPRQIEPDITRKTPDIFL"

1400

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/note="17 a nucleotides"

polyA_site

ORIGIN

Alignment Scores:

Pred. No.: 5.03e-147 Length: 1417

Score: 1538.00 Matches: 278

Percent Similarity: 95.75% Conservative: 15

Best Local Similarity: 90.85% Mismatches: 13

Query Match: 92.10% Indels: 0

DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x AB039916 (1-1417)

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Db 256 ATGCCGTCTCAGCGGATCTGGATCGGCAGATCGAGCATCTGATGGAGTGCAGGCTCTA 315

Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40

Db 316 CCGAGCGCGGATGTGAAGCGGCTTTCCGATCAGGCTAGGCGCATCTCTGTCGAAGAGTGG 375

Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlu 60

Db 376 AACGTTCAACCGGTGAAGTGTCCTGTTACGGTTTGTGGTGATATTACCGG 435

Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy 80

Db 436 CATCTGATTGAGCTTTTCGGATAGGAGAAACGCGCTGATACTAATTA 495

Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100

Db 496 GGAGATTATGTAGATCGTGGGTACTATTTCAGTGGAGACTGTTTCACITTT 555

Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120

Db 556 AAGTACGTTTATAGATAGAGATTACAATCTCAGGGGAAATCATGAGAG 615

Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 140

Db 616 ACTCAAGTGTATGCTTCTACGATGAATGCTTGAGAAAGTATGGAATGC 675

Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGlu 160

Db 676 AAATCTTTTACCGACTTGTGTTGATTATTATCTCTGACCGCCTTATTGCA 735

Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisAl 180

Db 736 TTCGTGTTGATGAGAGGTCCTCGCCATCTTTGGATACACTGGATAATAT 795

Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp 200

Db 796 GATCGCATACAGGAGGTTCACATGAGGACCGATGTCGGATCTCTGTG 855

Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh 220

Db 856 GATGATCTGTTGTTGGTGGGAATATCTCCAGAGGTGCTGGATATACATT 915

Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240

Db 916 ATAGCTGCCAGTTCATCAATACATAAATGGTCTCTCACATGATATCTAGAGC 975

Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh 260

Db 976 GTGATGGAGAGATACAAATGGTGGCAGGAGAAAGTATGTTGACTGTTT 1035

Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGlu 280

Db 1036 AATTACTCTACCGATGTGGGAATATGCTGCGATTCTGGAAATTTGGGA 1095

Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300

Db 1096 CAGAAATTTTCTGCAGTTTGATCCAGCTCCGAGGCAATTTGACGCTGACAC 1155

Qy 301 ThrProAspTyrPheLeu 306

Db 1156 ACACCAAGATTATTTTGG 1173

RESULT 5

AY325817

LOCUS

DEFINITION

Lycopersicon esculentum protein phosphatase 2A catalytic (PP2Ac) mRNA, complete cds.

ACCESSION

AY325817

VERSION

AY325817.1 GI:34398260

KEYWORDS

Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE

1 (bases 1 to 1380)

AUTHORS

He, X., Anderson, J.C., Pozo Od, O., Gu, Y.Q., Tang, X., and Silencing of subfamily I of protein phosphatase 2A cDNAs results in activation of plant defense response

TITLE

subunits results in activation of plant defense resp

QY	141	LysTyPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGI	le 160
Db	690	AAATATTTTCACTGATCTCTTTGATTATCTTACCATTGACGGCACTCATAGA	TA 749
QY	161	PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIrl	eu 180
Db	750	TTCTGTTTGCATGGAGGACTCTCACCATCCCTTGATACACTTGTGATAACAT	TG 809
QY	181	AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr	ro 200
Db	810	GACCGTATACAAGAGGTGCCACATGAAGGGCCGATGTGTGATCTCCTATG	CA 869
QY	201	AspAspArgCysGlyTrpGlyIleSerProArgGlyValaGlyTyrThrPh	sp 220
Db	870	GACGATCGCTGTGGTGGGGAATATCACCCTCGGGGGCTGGGTATACATTT	AT 939
QY	221	IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValaAlaArgAl	eu 240
Db	930	ATAGCATCTCAGTTTAATCACACTAATGGTCTCTCACTGATTTCTAGAGC	IT 989
QY	241	ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh	ro 260
Db	990	GTCAATGGAAGGTTTAAATTTGGTGTGACGATAAGAAATGTTGTAACAGTATT	CA 1049
QY	261	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGll	sn 280
Db	1050	AACTATVTGTATCGCTGTGCTAATATGGCTGCAATCTCTAGAATAAGTGA	AG 1109
QY	281	ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa	ys 300
Db	1110	CAGAATTTCTTCAGTTTGACCCAGCTCCACGACAGATTGAGCCTGATAC	AG 1169
QY	301	ThrProAspTyrPheLeu 306	
Db	1170	ACTCCAGACTACTTCTTG 1187	
RESULT 6			
LOCUS	FSY298829	1497 bp mRNA linear	PR-2005
DEFINITION	Fagus sylvatica mRNA for protein phosphatase 2A (pp2)
ACCESSION	AJ298829		
VERSION	AJ298829.1 GI:10638984		
KEYWORDS	pp2A-1 gene; protein phosphatase 2A.		
SOURCE	Fagus sylvatica (European beech)		
ORGANISM	Fagus sylvatica		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e		phyta; edons;
AUTHORS	1. .1497		
TITLE	Gonzalez, M., Nicolas, C., Lorenzo, O., Nicolas, G. and Characterization and expression of a protein phosphat regulated by GA3 in dormant Fagus sylvatica seeds		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1497)		
AUTHORS	Nicolas, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-OCT-2000) Nicolas C., Fisiologia Veget de Salamanca, Plaza Doctores de la Reinas/n, 37007 Sa		ersidad SPAIN
FEATURES	Location/Qualifiers		
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CDS	258. .1178		
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	/codon_start=1		

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/db_xref="InterPro:IPR004843"
/db_xref="UniProt:TrEMBL:Q9FSV3"
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ORIGIN

Alignment Scores:
Pred. No.: 9,07e-146 Length: 1497
Score: 1526.00 Matches: 274
Percent Similarity: 95.42% Conservative: 18
Best Local Similarity: 89.54% Mismatches: 14
Query Match: 91.38% Indels: 0
DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x FSV298829 (1-1497)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
DB 258 ATGCGGTGCGACTCGGATCGGACGTCAGATCGAGCATCTGTGGAGTGCAGCGCGTTG 317
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
DB 318 CCGGAGCGGAGGTGAACGGCTTCGATCAGCGAGCGAGCGCATCTGTGGAGGAGTGG 377
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 378 AAGGTACAAACCGTGAAGTCCCGGTGACGGTGCAGTGTATCCACGGCGAGTCTTAC 437
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMet 80
DB 438 GATCTCATCGAGCTCTTCGAGATAGAGGAAATGCTCCGATACCAATTTATCTCTCATG 497
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
DB 498 GAGATATTATGATGCTGGTACTACCCAGTTGAGACTGTTTACACTTTTGTGGCTCTG 557
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 558 AAAGTTCTGTTATAGATAGGATCAATTTCTAGAGGGAATCATGAGAGCGCGCAATA 617
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 618 ACTCAAGTGTATGGTTTTTATACCAAGTCTTGAGAAATACGGAATGCCAAGCTGTGG 677
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DB 678 AAGTCTTCACCACTATTGATATCTACCCCTTACAGCCCTTATTGAGAGTCAGATC 737
QY 161 PheCysLeuHisGlyCysLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 738 TTCTGTTTCATGGAGTCTTTCCACCATCTTTGGATACGTTGGATAATATTCAGCCCTG 797
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 798 GACCGGTATACGAGGTTCCACACGAAGGACCAATGTGTGACCTCTTATGGTCTGATCCT 857
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 858 GATGACCGATGTGGTGGGGAATATCTCTCTGTTGCTGGATATACATTTCGACAGGAT 917
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 918 ATAGTGTCTCAGTTCAACCATCAATAGGGCTCACACTGATTTTCAAGAGCCACCAGCTT 977

QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh 260
DB 978 GTTATGAAGGGTTCAATTGGTGTGAGATAGAAATGTGGTACTGTATT 1037
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DB 1038 AACTATTGTTACCTGTGGGAATATGCTGCAATCTGGAGATGGGGA 1097
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300
DB 1098 CAGAATTTCTGCAAGTTGATCCAGCCCCCGACAAATTTGAGCCTGACAC 1157
QY 301 ThrProAspTyrPheLeu 306
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RESULT 7
AY093267
LOCUS
DEFINITION
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ACCESSION
AY093267
VERSION
AY093267.1 GI:20259837
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Euphyllophyta; Magnoliophyta; eudicotyledons; core eukaryotes; eurosids II; Brassicales; Brassicaceae; Arabidopsis
1 (bases 1 to 1092)
REFERENCE
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamakawa, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (26-MAR-2002) DNA Sequencing and Technology: Stanford University, 855 California Avenue, Palo Alto, USA
e-mail for correspondence: arab@sequence.stanford.edu
RIKEN Genomic Sciences Center (GSC) members carried out collection and clustering of RAFL cDNAs (RAFL cDNA: Arabidopsis Full-length cDNA): Seki, M., Narusaka, M., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGSC (SSP) Consortium members carried out sequencing and annotation of the RAFL cDNAs: Southwick, Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., Pham, Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chu, Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shimada, Y., Ecker, J., Theologis, A. and Davis, R.W.
Southwick, A. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and (SSP/Stanford) contributed equally to this work as follows:
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/db_xref="taxon:3702"
/chromosome="1"
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1. .1092
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CDS

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/gene="Atlg10430"
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ORIGIN

Alignment Scores:
Pred. No.:      1.55e-145      Length:      1092
Score:          1522.00      Matches:      274
Percent Similarity: 95.10%      Conservative: 17
Best Local Similarity: 89.54%      Mismatches:   15
Query Match:      91.14%      Indels:       0
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US-10-764-259-13 (1-306) x AY093267 (1-1092)

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Db 1 ATCCGTCGAACGGAGATCTGGACCGTCAGATCGAGCAGCTGATGGAGTGTAAACCGTTA 60

QY 21 SerGluLeuGlnValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
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QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
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Qy      161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisileArgAlaLeu 180
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Qy      261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluileAspGluThrMetAsn 280
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RESULT 10
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LOCUS   Ab039917 1475 bp mRNA linear PLN 15-MAR-2000
DEFINITION
Vicia faba vFP2Ac-2 mRNA for type 2A protein phosphatase-2,
complete cds.
ACCESSION
AB039917
VERSION
AB039917.1 GI:7248360
KEYWORDS
vFP2Ac-2; type 2A protein phosphatase-2.
SOURCE
Vicia faba (fava bean)
ORGANISM
Vicia faba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Vicia.
REFERENCE
1 (bases 1 to 1475)
AUTHORS
Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.
TITLE
Type 2A protein phosphatase from guard cells of Vicia faba
JOURNAL
Published Only in Database (2000)
REFERENCE
2 (bases 1 to 1475)

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AUTHORS Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAR-2000) Toshihori Kinoshita, Kyushu
 Graduate School of Sciences; Ropponmatsu 4-2-1, Fuku
 810-8560, Japan (E-mail:toshirc@box.nc.kyushu-u.ac
 Tel:81-92-726-4763(ex.4763), Fax:81-92-726-4644)

FEATURES

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 DB: Gaps: 0
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 Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuileGl

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LLVALKV
ALIESQV
SAGYTFG
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TG 314rp 40
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GG 374is 60
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AC 434et 80
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TG 494eu 100
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RESULT 11

AY087557

LOCUS AY087557 1261 bp mRNA linear PLN 14-APR-2003

DEFINITION Arabidopsis thaliana clone 36621 mRNA, complete sequence.

ACCESSION AY087557

VERSION AY087557.1 GI:21406295

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Haas, B.J., Volfovsky, N., Town, C.D., Troupkhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.

TITLE Full-length messenger RNA sequences greatly improve genome annotation

JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)

PUBMED 12093376

REFERENCE 2 (bases 1 to 1261)

AUTHORS Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

TITLE Full-length cDNA from Arabidopsis thaliana

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1261)

AUTHORS Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

TITLE Direct Submission

JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A

sequence is considered to be 3'-truncated if it lacks C-terminal end of the encoded protein. Please note that sequences are derived from the Ws or Llaer ecotypes and may contain polymorphisms when compared to sequences Genset carried out the library production and sequencing full-length clones. Ceres, Inc. carried out the cloning, 5' sequences, selection of clones, and sequence assembly

FEATURES

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153. .1073

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ORIGIN

Alignment Scores:

Pred. No.: 1,22e-144 Length: 1261

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Best local Similarity: 89.22% Mismatches: 16

Query Match: 90.66% Indels: 0

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US-10-764-259-13 (1-306) x AY087557 (1-1261)

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Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly

Db 273 AATGTTCAACCGTTAAGTGTCCGTTACGGTATGCGCGGATATCCATGG

Qy 61 AspLeuIleGluLeuPheArgIleGlyCysAlaProAspThrAsnTyr

Db 333 GACCTAATTGAGCTATTTTCGTATTGGTGGTAAATGCTCTGATCTAATTA

Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu

Db 393 GGAGATTATGATCGTGGCTACTATTCTGTAGAACAGTCTCTCTATT

Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySer

Db 453 AAGTGTGCTTACAGGACAGACTTACGATCTCGAGGGAATCATGAGAG

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Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle

Db 633 TTCTGTTGTCATGGAGGCGTTTTCACCTTCTCTGGATCTCTTGTGACATAT

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3EYNVQP
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ALIESQV
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AILEIG


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DEFINITION
ACCESSION AX506010
VERSION   AX506010.1  GI:23387247
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SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS  Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
TITLE    Stress-regulated genes of plants, transgenic plants containing
JOURNAL  Patent: WO 0216655-A 705 28-FEB-2002;
          The Scripps Research Institute (US); Syngenta Participations AG
          (CH)
FEATURES
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ORIGIN
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Score:          1508.00      Matches:      272
Percent Similarity: 94.4%      Conservative: 17
Best Local Similarity: 88.8%      Mismatches: 17
Query Match:    90.30%      Indels:      0
DB:             6             Gaps:        0

US-10-764-259-13 (1-306) x AX506010 (1-921)

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Qy      21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
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Qy      221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240
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VERSION   AY096543.1  GI:20465466
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          1 (bases 1 to 952)
REFERENCE Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,B.,
AUTHORS   Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., C

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Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

Arabidopsis Open Reading Frame (ORF) Clones

Unpublished
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 952)
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

Direct Submission

Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan

Street, Albany, CA 94710, USA

COMMENT
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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3'UTR

ORIGIN

Alignment Scores:

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Query Match: 90.30% Indels: 0
DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x AY096543 (1-952)

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DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACACGCTAATGGAGTG; TA 60
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal; p 40
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QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly; LS 60
DB 121 AATGTTCAACCGTTAAGTGTCCGGTTACGGTATGCGGCGATATCCATGG; AT 180
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy; AT 80
DB 181 GACCTAATTGAGCTATTTCGTATTGGTGAATGCTCTCTGATCTAATTA; TG 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe; au 100
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